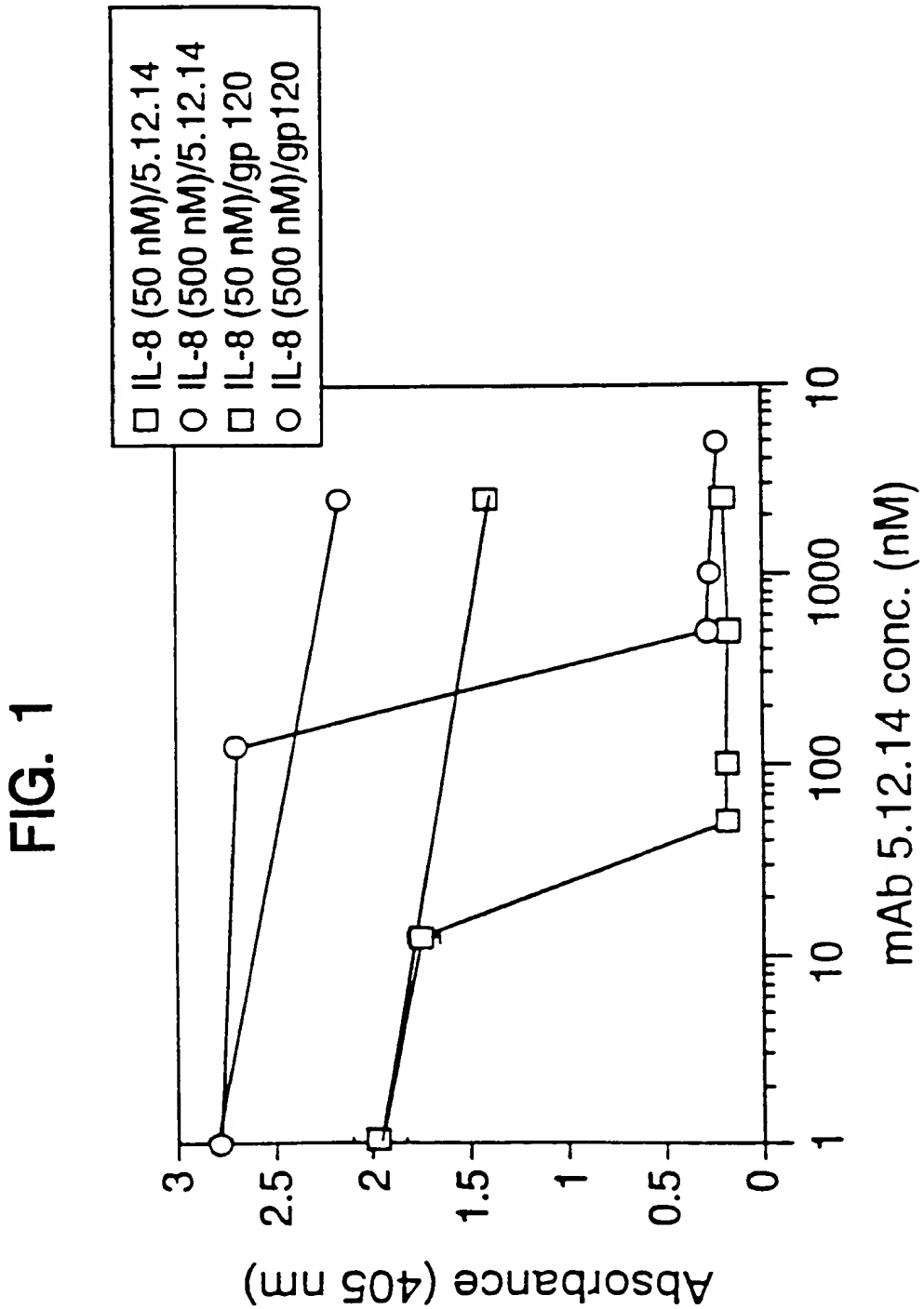
FIG. 1



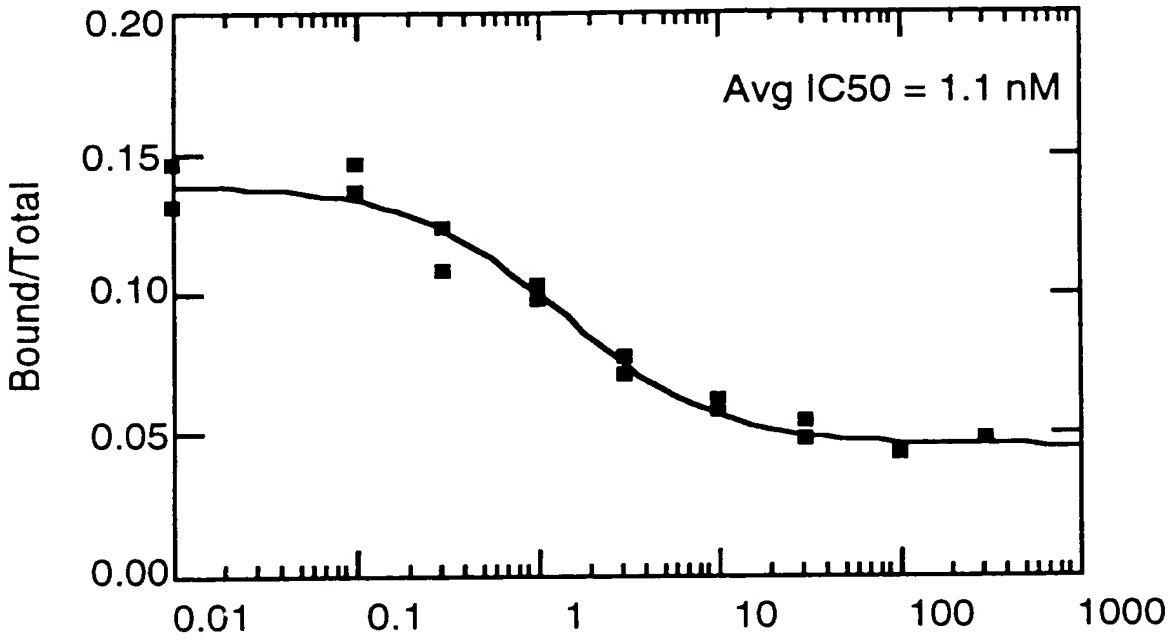


FIG. 2

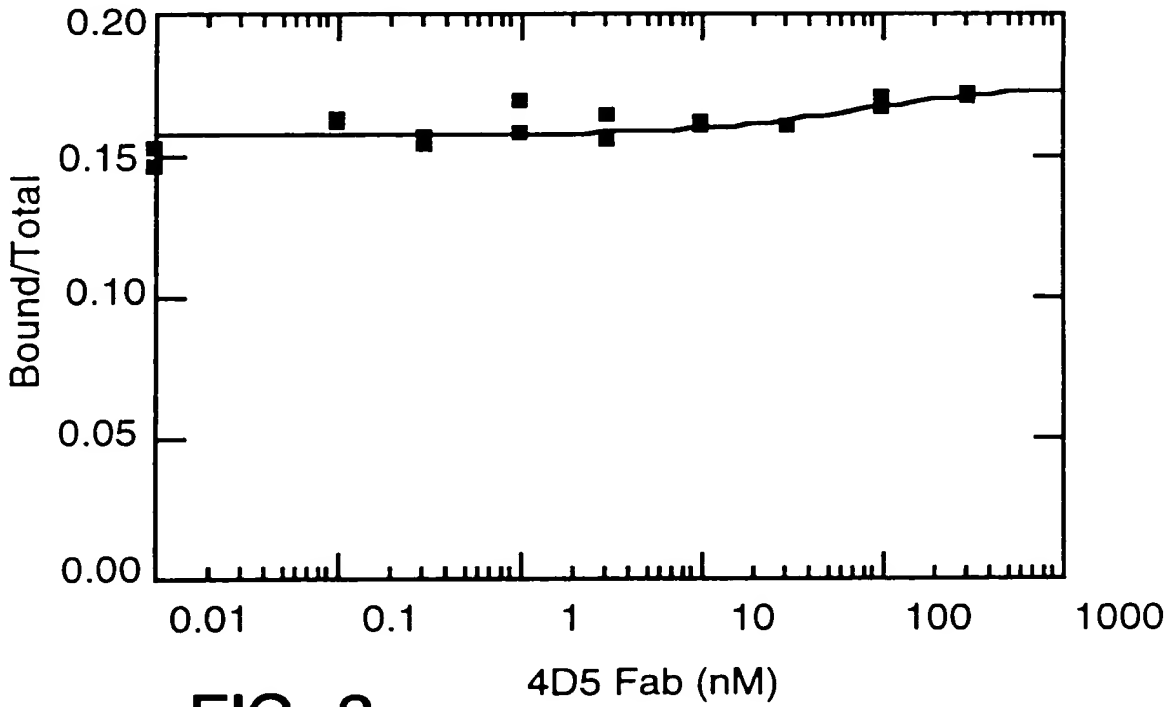


FIG. 3

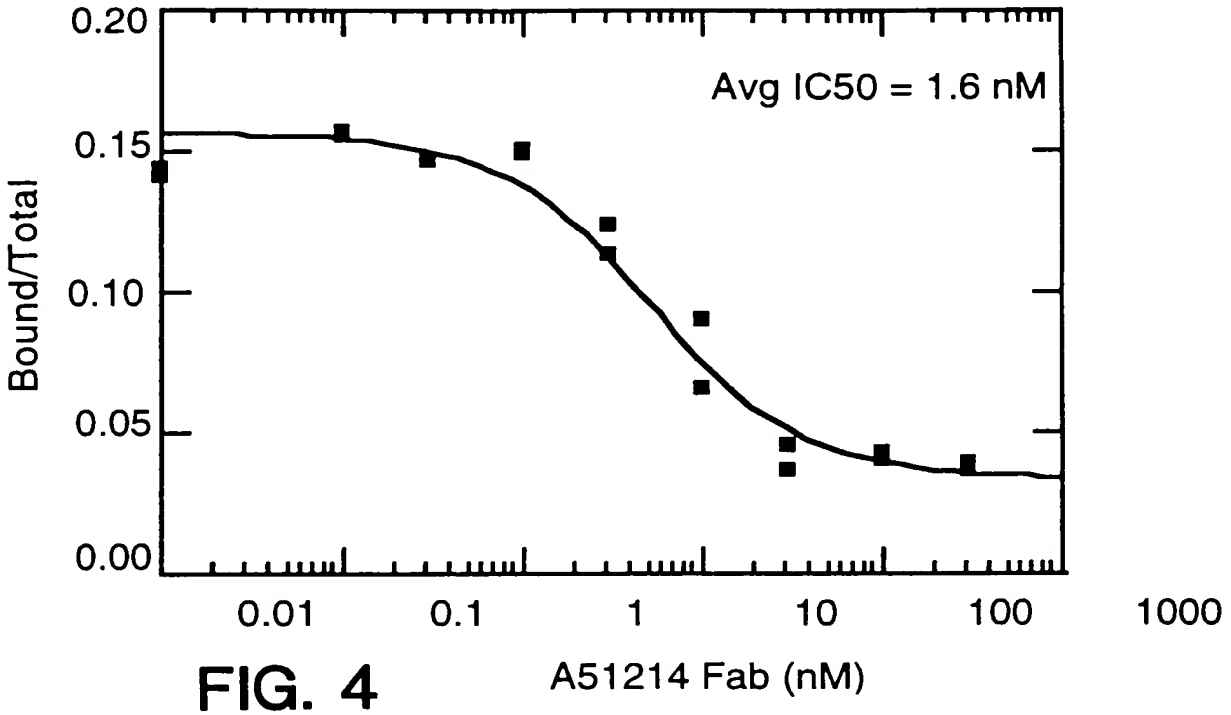


FIG. 4

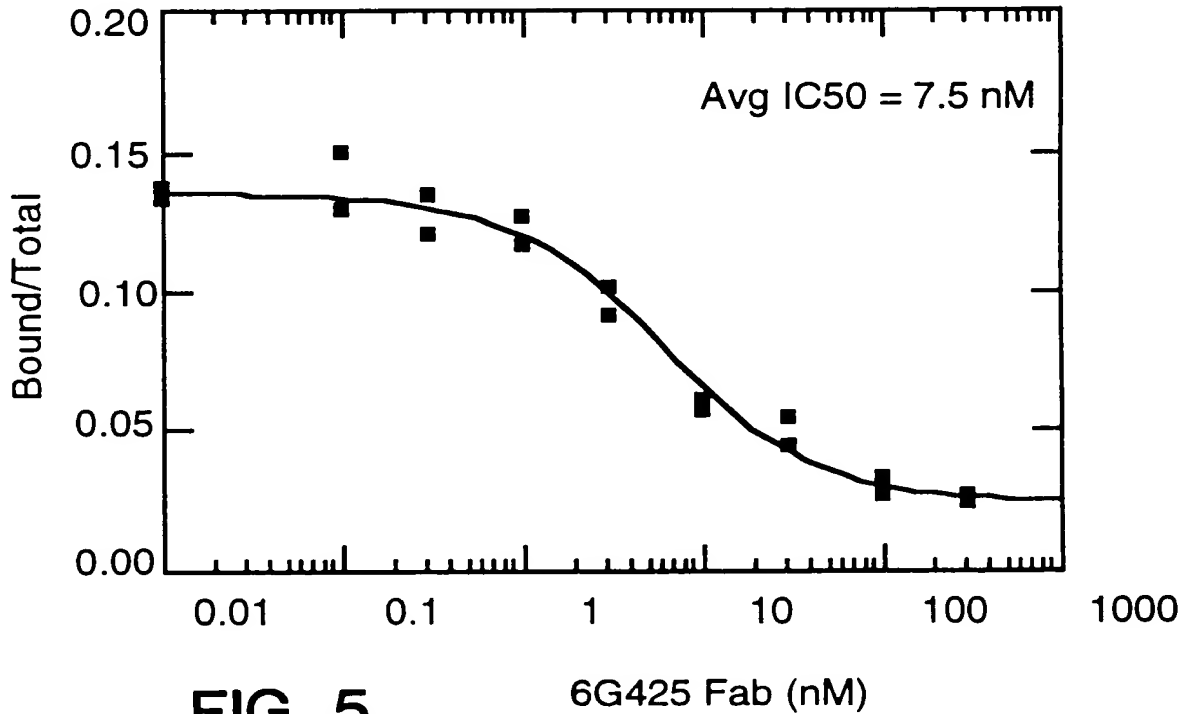


FIG. 5

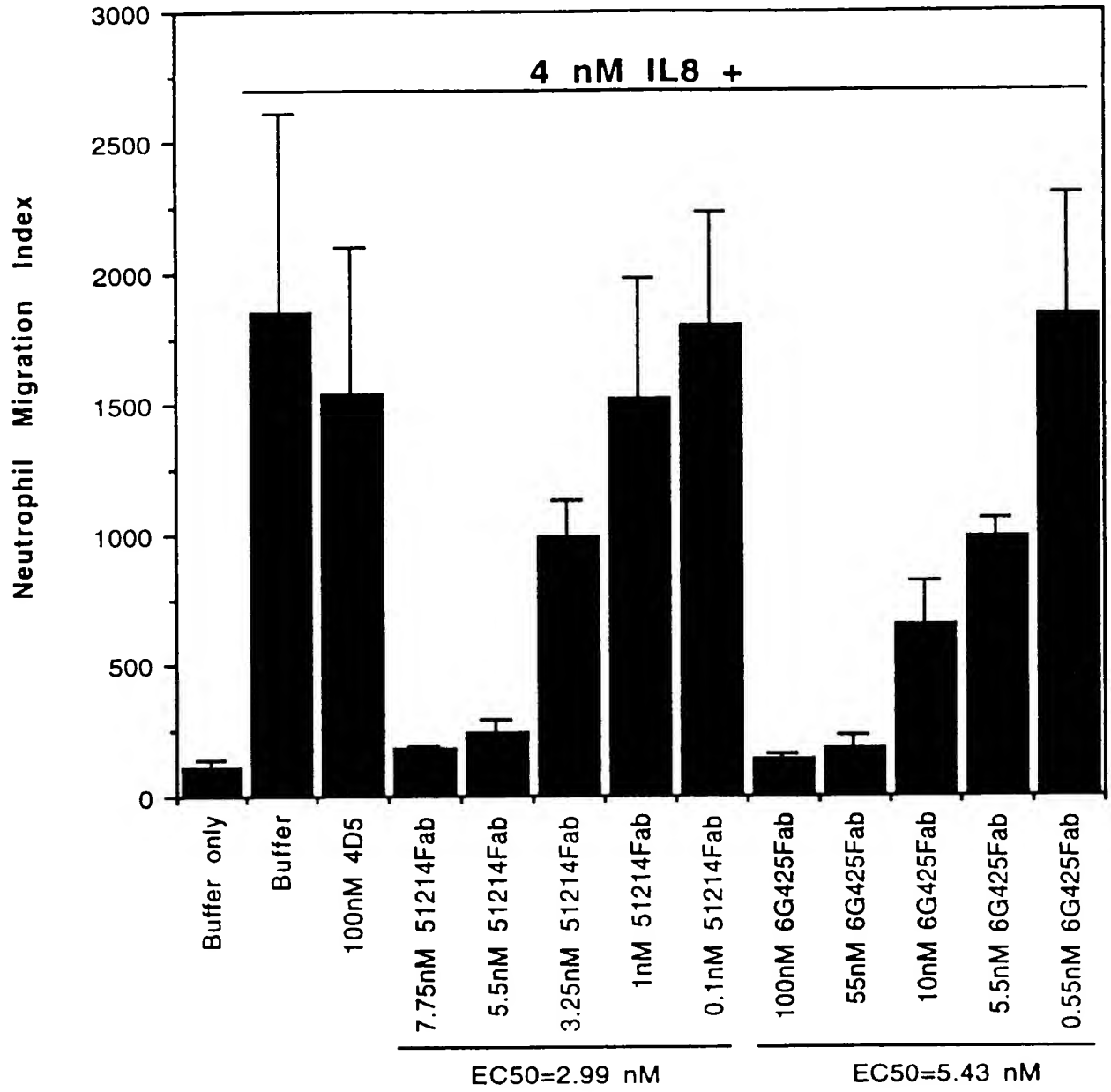


FIG. 6

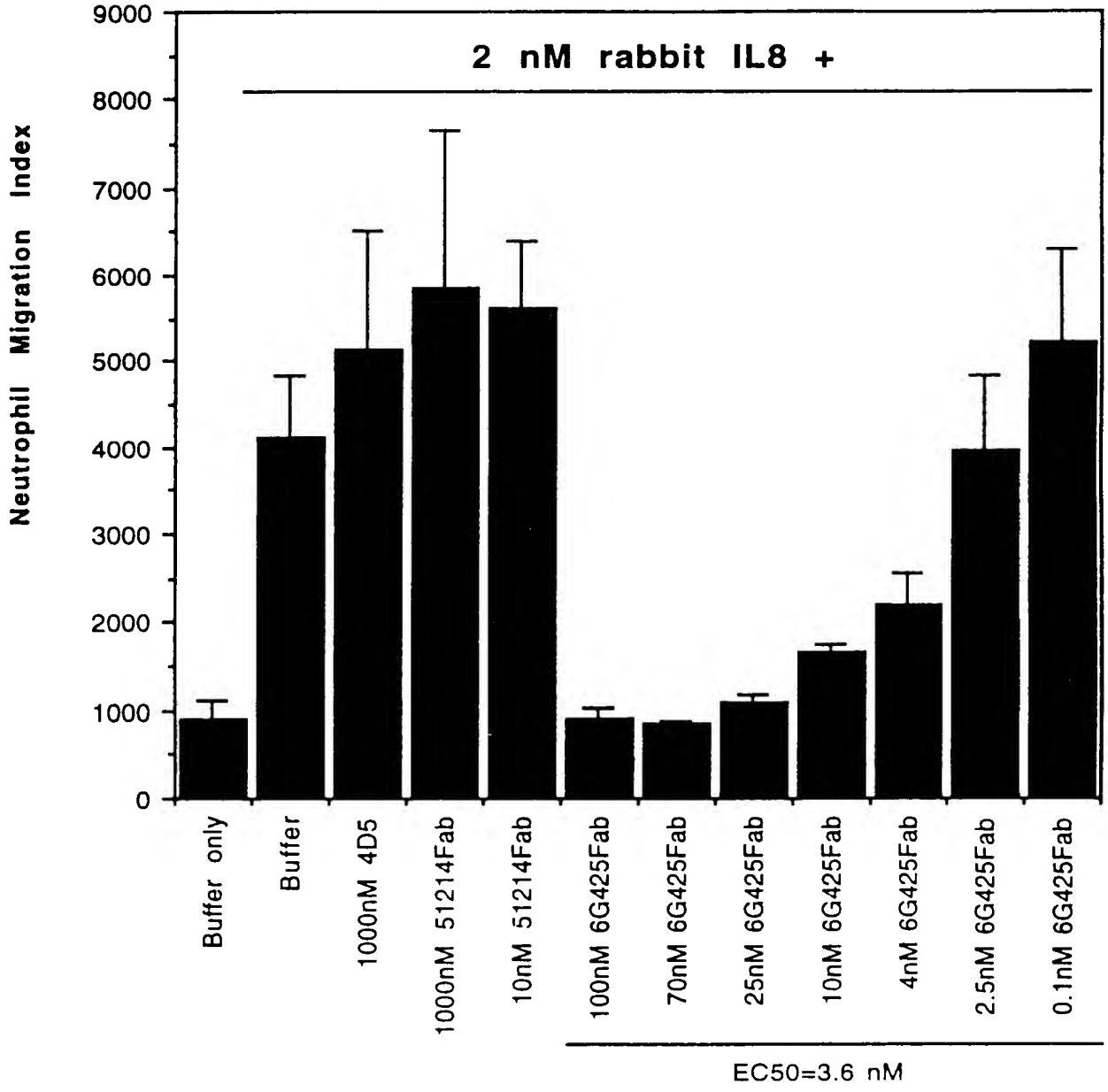


FIG. 7

FIG. 8

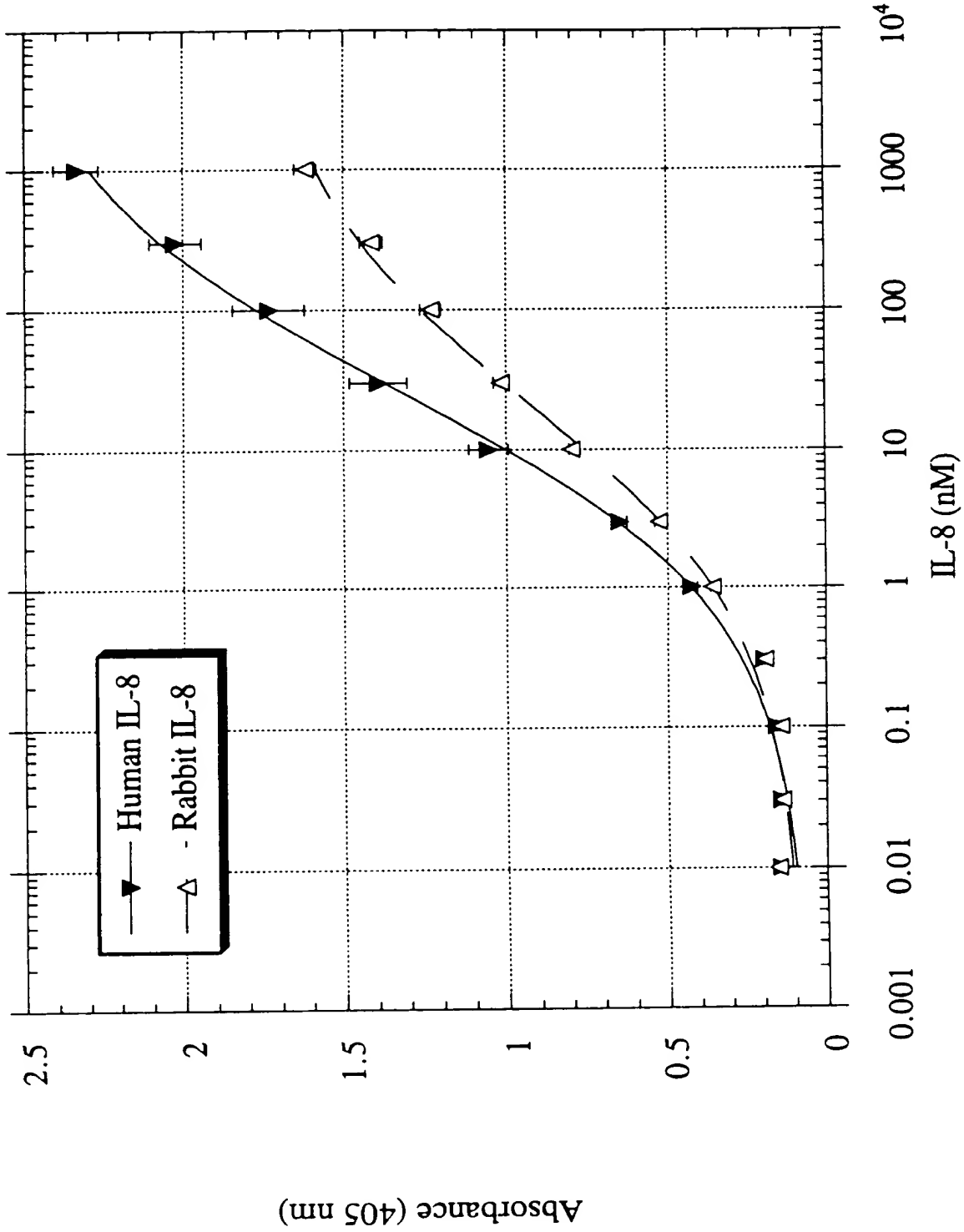


FIG. 9

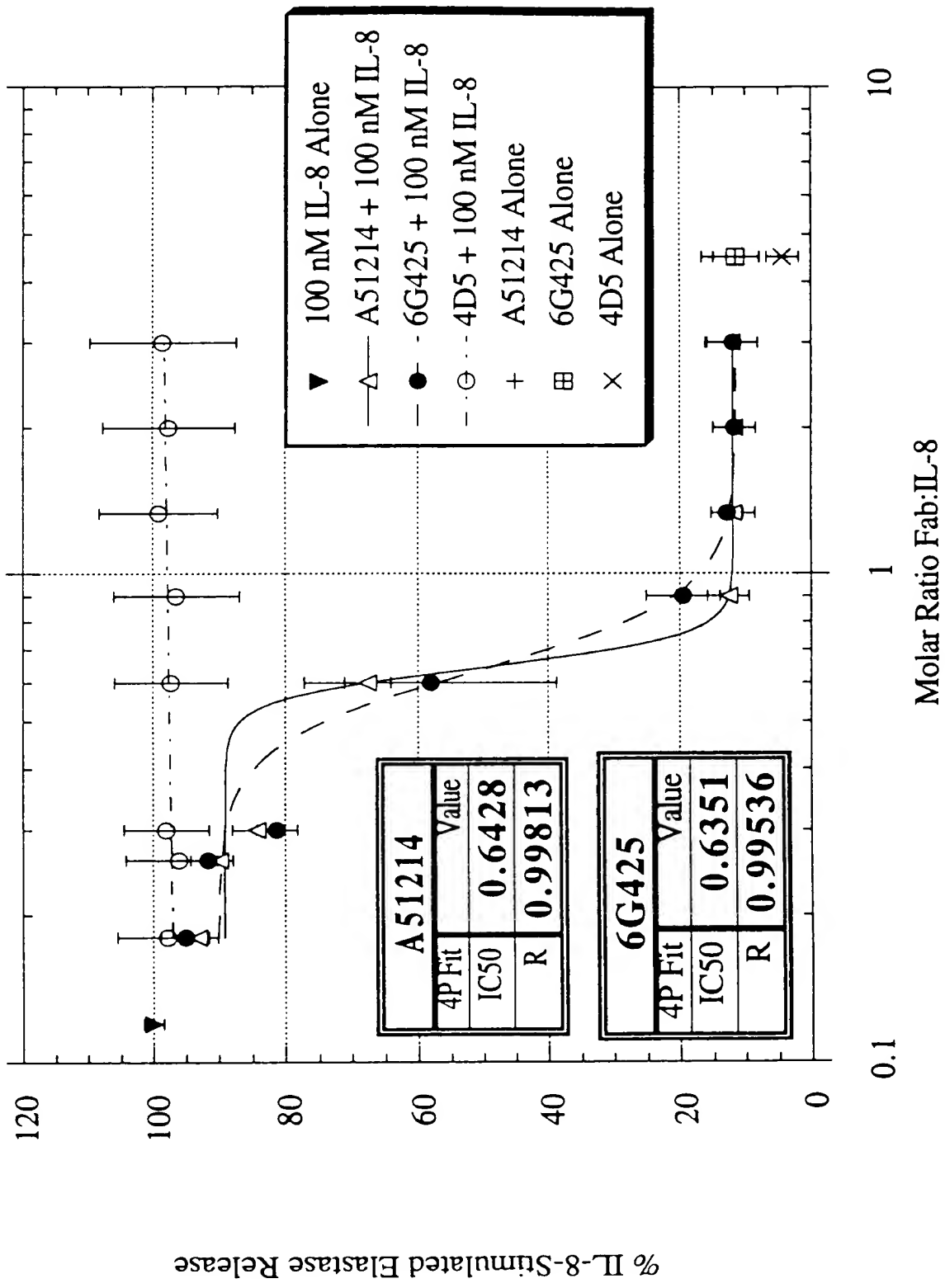
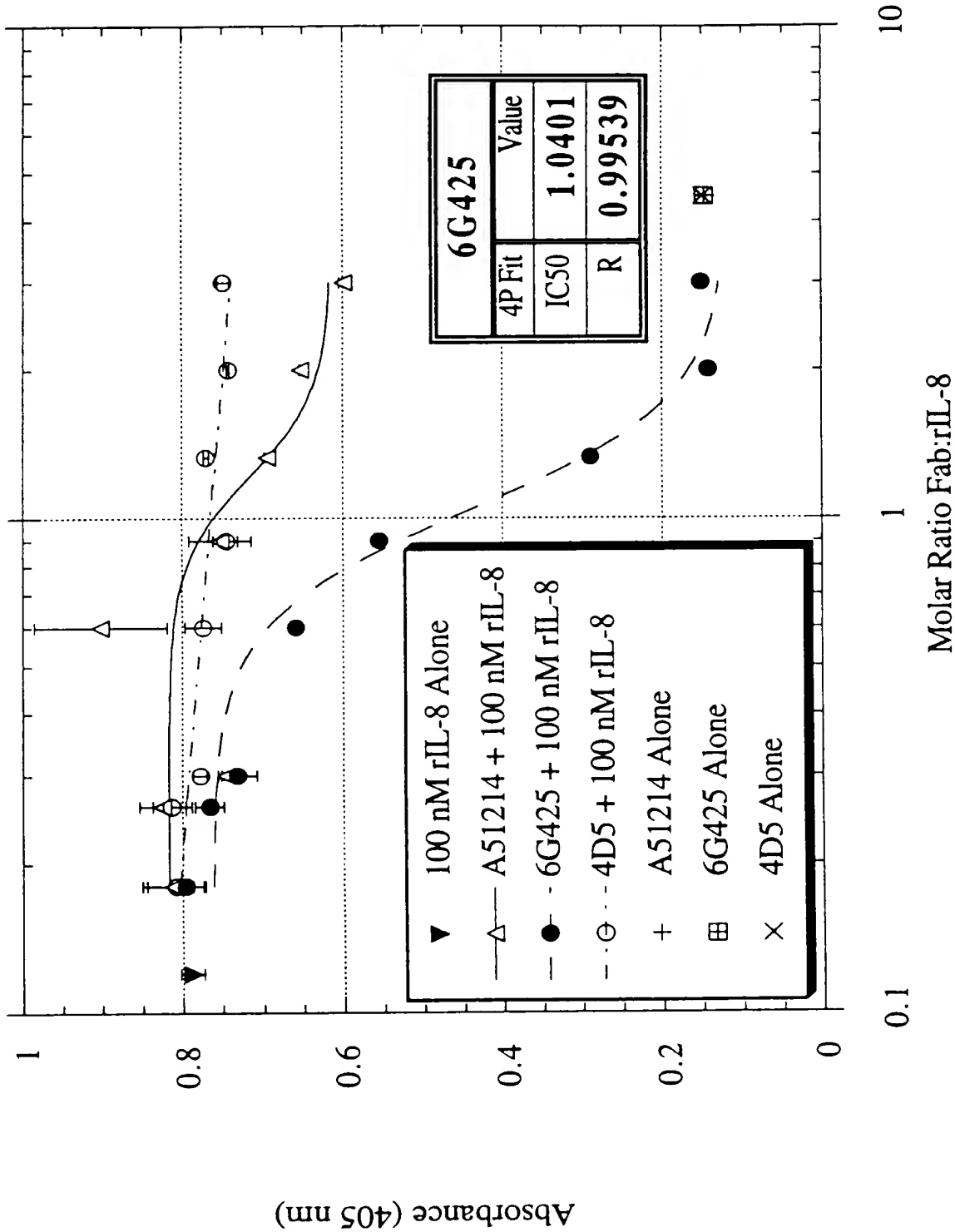


FIG. 10



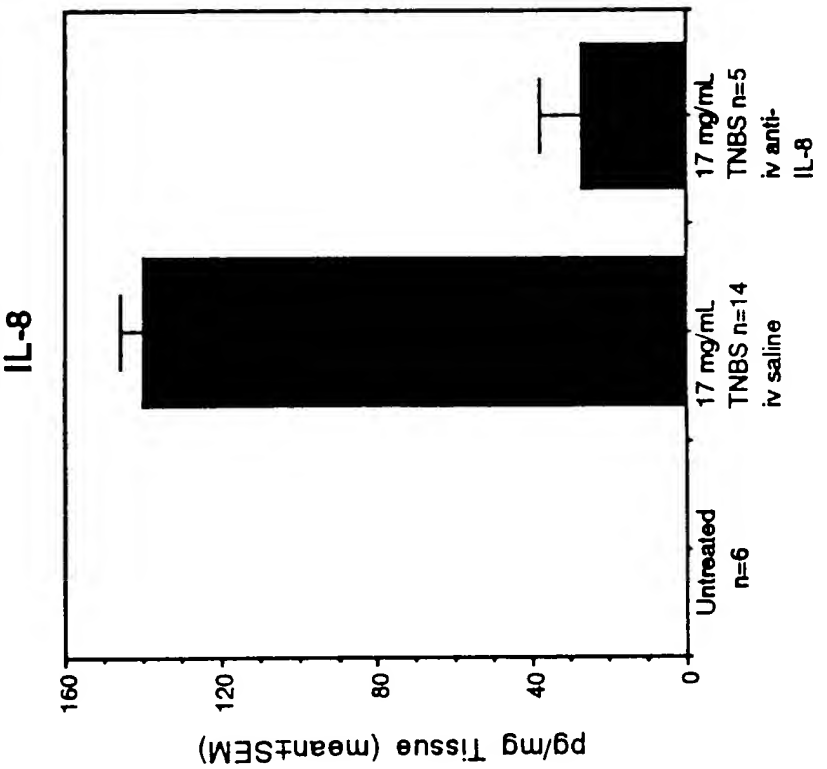


FIG. 11B

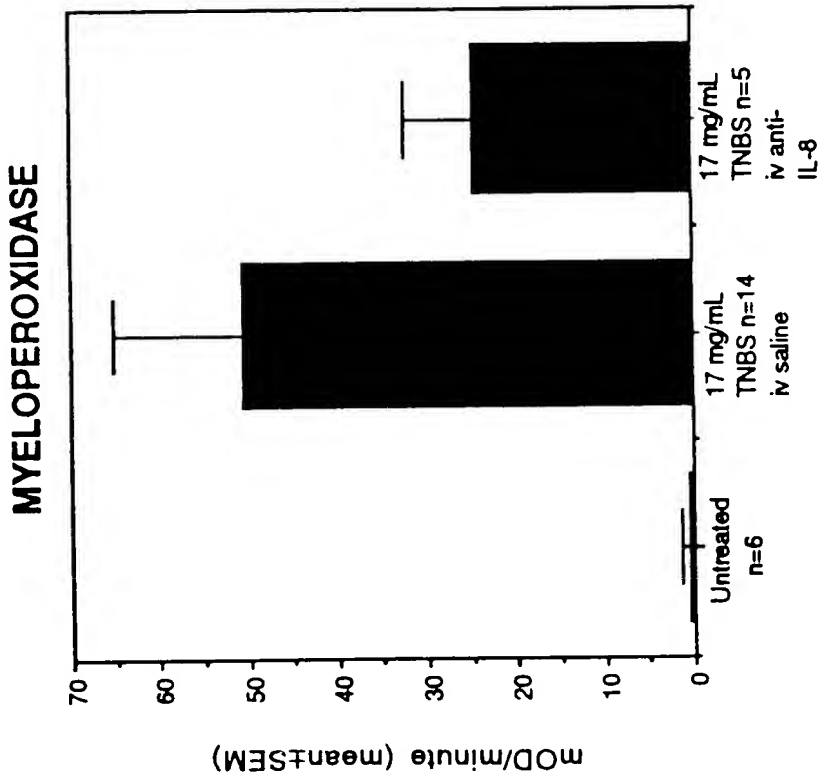


FIG. 11A

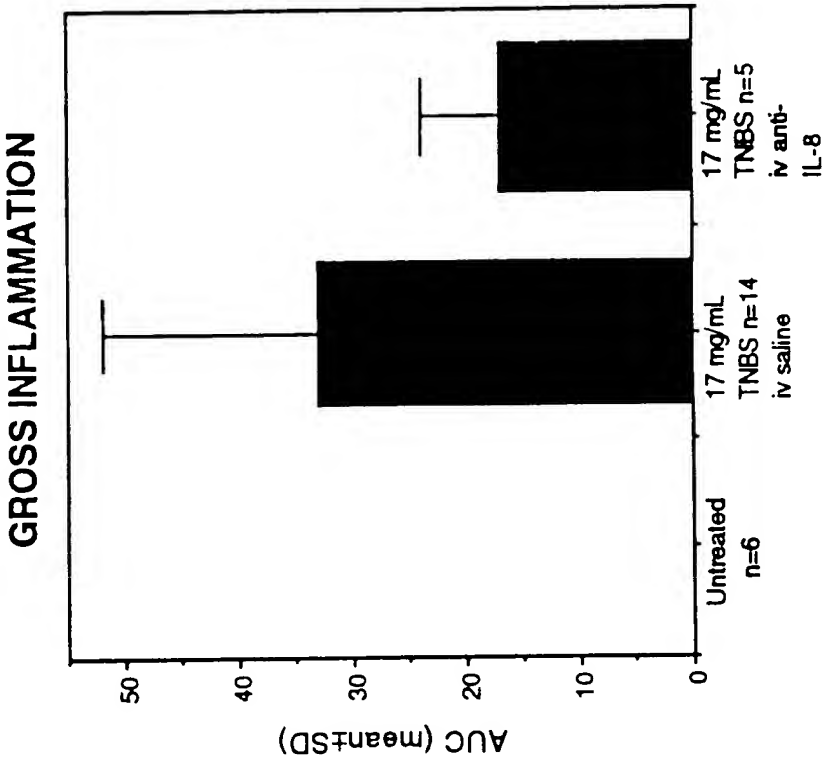


FIG. 11D

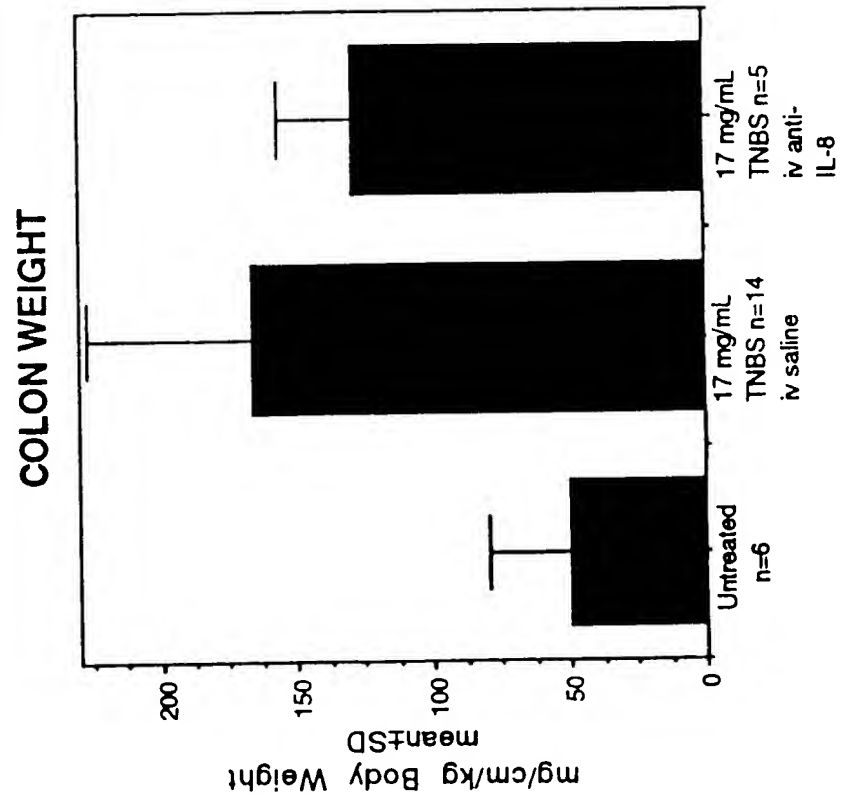


FIG. 11C

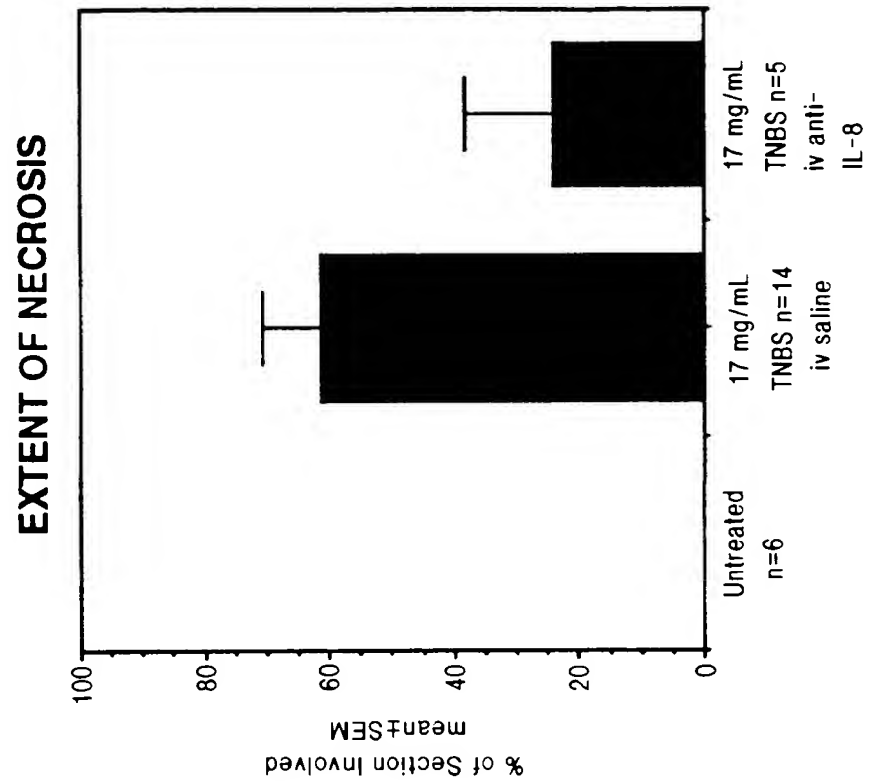


FIG. 11F

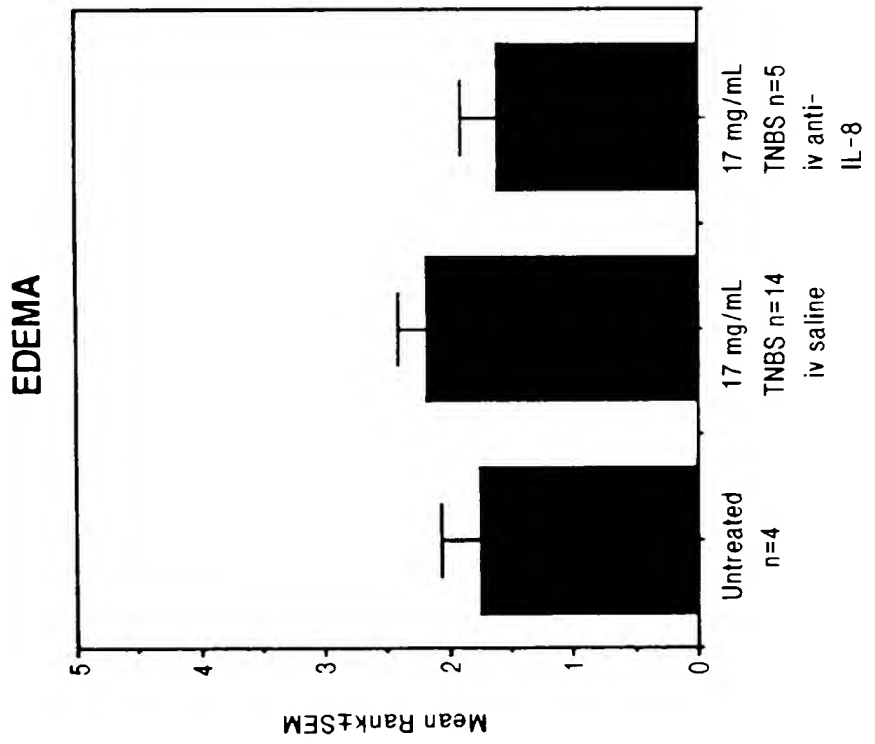


FIG. 11E

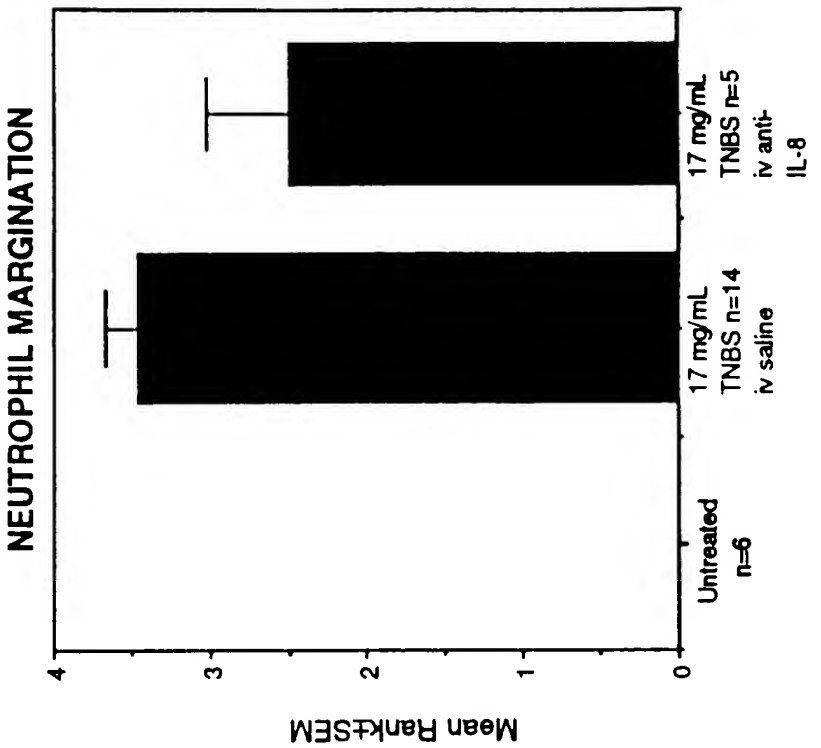


FIG. 11H

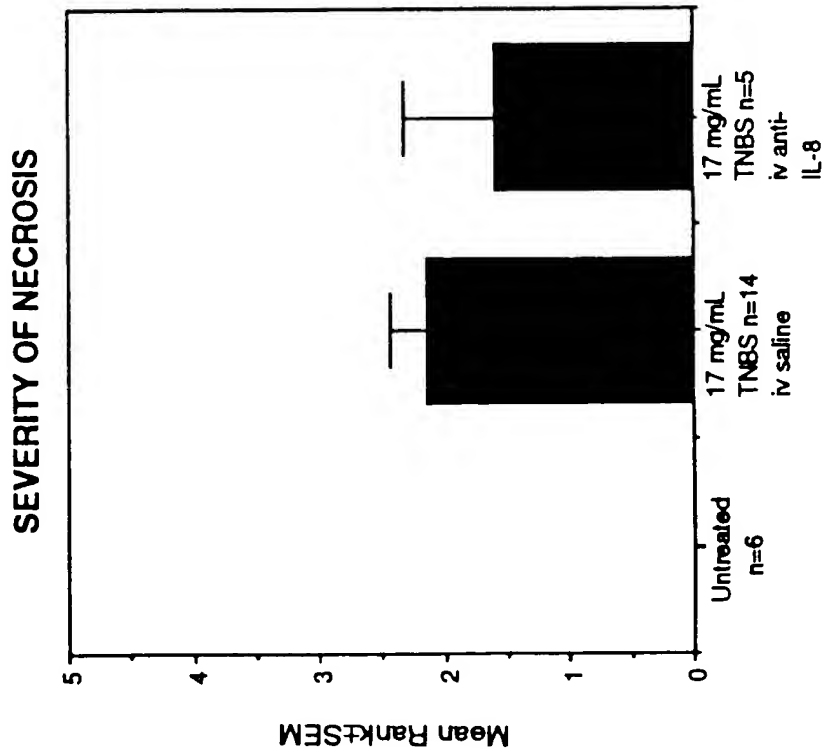


FIG. 11G

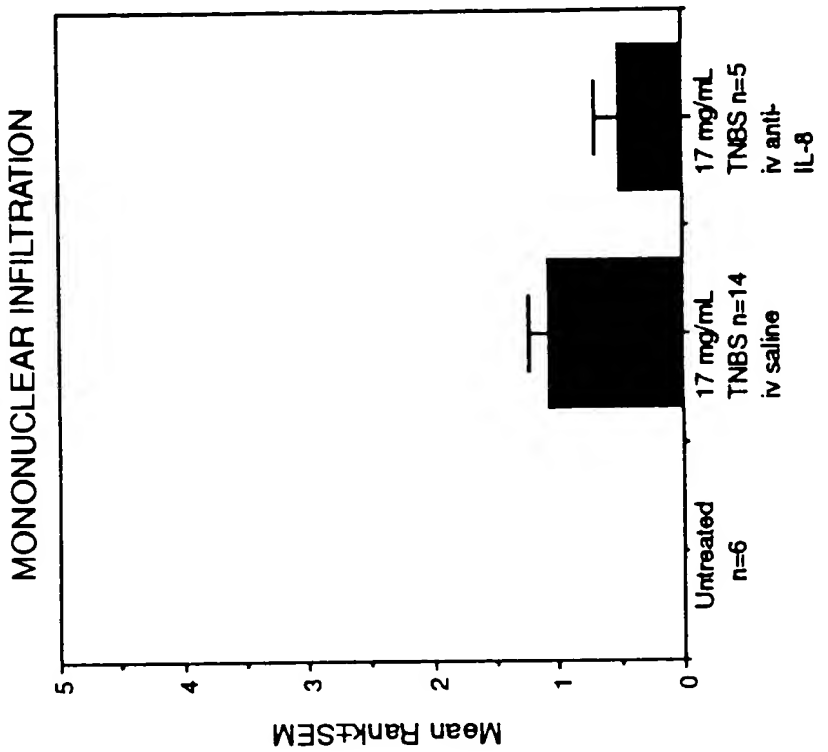


FIG. 11J

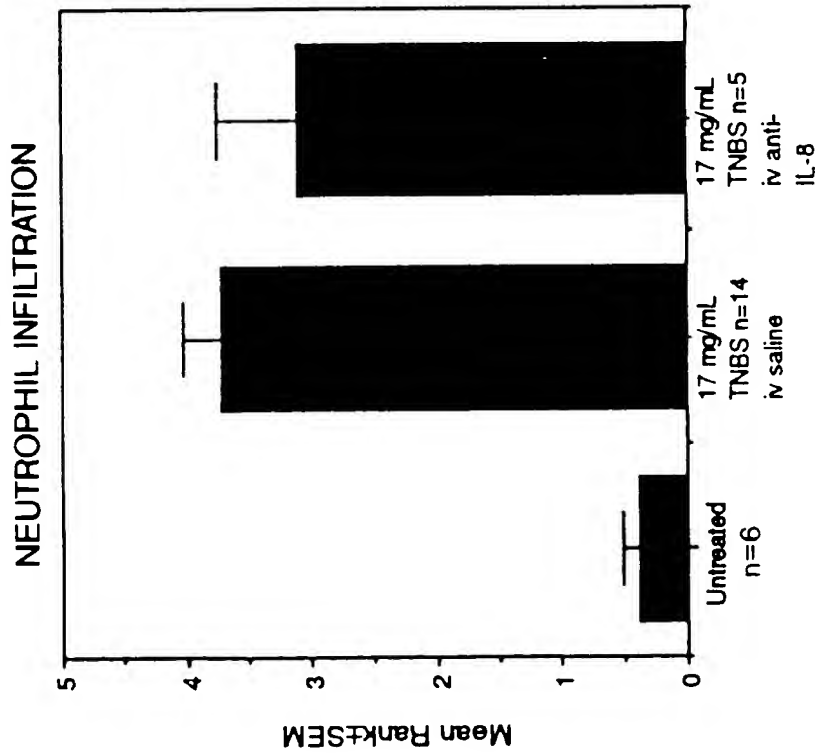


FIG. 11I

FIG. 12

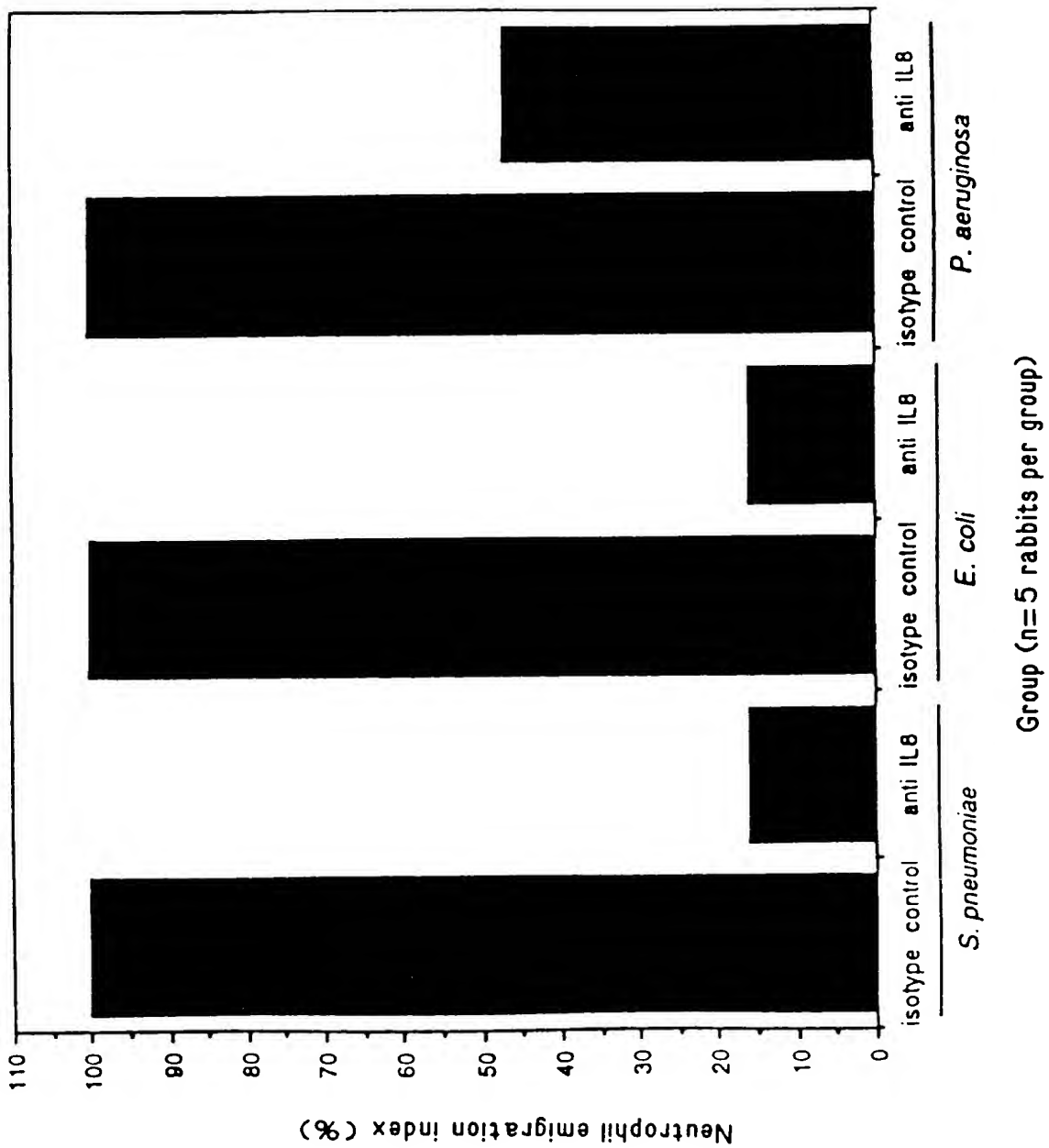


FIG. 13

Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACTGTTCAGGACGCC 3' (SEQ ID NO.1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3' (SEQ ID NO.2)

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3' (SEQ ID NO.3)

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3' (SEQ ID NO.4)

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3' (SEQ ID NO.5)

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3' (SEQ ID NO.6)

FIG. 14

Light chain forward primer

SL001A-2 35 mer

5' ACAAACGCGTACGCT GACATCGTCATGACCCAGTC 3' (SEQ ID NO.7)
T T T (SEQ ID NO.8)
A (SEQ ID NO.9)

Light chain reverse primer

SL001B 37 mer

5' GCTCTTCGAATG GTGGGAAGATGGATACAGTTGGTGC 3' (SEQ ID NO.10)

FIG. 15

Heavy chain forward primer

SL002B 39 mer

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3'			(SEQ ID NO.11)
	T	C	(SEQ ID NO.12)
	G		(SEQ ID NO.13)
	A		(SEQ ID NO.14)

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3'			(SEQ ID NO.11)
	T		(SEQ ID NO.15)
	A		(SEQ ID NO.14)
	G		(SEQ ID NO.13)

```
  1 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC
    CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCCAGTCG
  1 D  I  V  M   T  Q  S   Q  K  F   M  S  T  S   V  G  D   R  V  S

 61 GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG CCTGGTATCA ACAGAAACCA
    CAGTGGACGT TCCGGTCAGT CTTACACCCA TGATTACATC GGACCATAGT TGTCTTTGGT
 21 V  T  C  K   A  S  Q  N  V  G   T  N  V  A   W  Y  Q   Q  K  P
               *   *  *  *  *  *  *   *  *  *  *
                                CDR #1

121 GGGCAATCTC CTAAAGCACT GATTTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT
    CCCGTTAGAG GATTTCGTGA CTAAATGAGC AGTAGGATGG CCATGTCACC TCAGGGACTA
 41 G  Q  S  P   K  A  L   I  Y  S   S  S  Y  R   Y  S  G   V  P  D
                                  *   *  *  *  *   *  *
                                          CDR #2

181 CGCTTCACAG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT
    GCGAAGTGTC CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAGTCGGT ACACGTCAGA
 61 R  F  T  G   S  G  S   G  T  D   F  T  L  T   I  S  H   V  Q  S

241 GAAGACTTGG CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT
    CTTCTGAACC GTCTGATAAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA
 81 E  D  L  A   D  Y  F   C  Q  Q   Y  N  I  Y   P  L  T   F  G  P
                              *  *   *  *  *  *   *  *  *
                                   CDR #3

301 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC CATCTTCCCA
    CCCTGGTTCG ACCTCAACTT TGCCCGACTA CGACGTGGTG GTTGACATAG GTAGAAGGGT
101 G  T  K  L   E  L  K   R  A  D   A  A  P  P   T  V  S   I  F  P

       BstBI
361 CCATTCGAA (SEQ ID NO.16)
    GGTAAGCTT
121 P  F  E   (SEQ ID NO.17)
```

FIG. 16

```
  1 TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG GAGGCTTAGT
    AAGATAACGA TGTTTGCGCA TGCGACTCCA CGTCGACCAC CTCAGACCCC CTCCGAATCA
  1                              E  V   Q  L  V   E  S  G  G   G  L  V

 61 GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT GGATTCATAT TCAGTAGTTA
    CGGCGGACCT CCCAGGGACT TTGAGAGGAC ACGTCGGAGA CCTAAGTATA AGTCATCAAT
 13  P  P  G   G  S  L  K   L  S  C   A  A  S   G  F  I  F   S  S  Y
                                                              *  *

                                                        CDR #1

121 TGGCATGTCT TGGGTTCGCC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTAA
    ACCGTACAGA ACCCAAGCGG TCTGAGGTCC GTTCTCGGAC CTCAACCAGC GTTGGTAATT
 33  G  M  S   W  V  R  Q   T  P  G   K  S  L   E  L  V  A   T  I  N
     *  *  *                                                 *  *  *

181 TAATAATGGT GATAGCACCT ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG
    ATTATTACCA CTATCGTGGA TAATAGGTCT GTCACACTTC CCGGCTAAGT GGTAGAGGGC
 53  N  N  G   D  S  T  Y   Y  P  D   S  V  K   G  R  F  T   I  S  R
     *  *  *   *  *  *  *   *  *  *   *  *  *

                      CDR #2

241 AGACAATGCC AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC
    TCTGTTACGG TTCTTGTGGG ACATGGACGT TTACTCGTCA GACTTCAGAC TCCTGTGTCG
 73  D  N  A   K  N  T  L   Y  L  Q   M  S  S   L  K  S  E   D  T  A

301 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT ACTGGGGCCA
    GTACAAAATG ACACGTTCTC GGGAGTAATC AAGCCGATGA ACCAAACCAA TGACCCCGGT
 93  M  F  Y   C  A  R  A   L  I  S   S  A  T   W  F  G   Y   W  G  Q
                    *      *  *  *   *  *  *   *  *  *   *

                                  CDR #3

361 AGGGACTCTG GTCACTGTCT CTGCAGCCAA AACAACAGCC CCATCTGTCT
    TCCCTGAGAC CAGTGACAGA GACGTCGGTT TTGTTGTCGG GGTAGACAGA
113  G  T  L   V  T  V  S   A  A  K   T  T  A   P  S  V  Y

        ApaI
411    ATCCGGG  (SEQ ID NO.18)
       TAGGCCC
130      P      (SEQ ID NO.19)
```

FIG. 17

FIG. 18

VL.front 31-MER

5' ACAAACGCGTACGCTGATATCGTCATGACAG 3' (SEQ ID NO.20)

VL.rear 31-MER

5' GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG 3' (SEQ ID NO.21)

VH.front.SPE 21-MER

5' CCACTAGTACGCAAGTTCACG 3' (SEQ ID NO.22)

VH.rear 33-MER

5' GATGGGCCCTTGGTGGAGGCTGCAGAGACAGTG 3' (SEQ ID NO.23)

```
  1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA TGTCCACATC AGTAGGAGAC
    CGCATGCGAC TATAGCAGTA CTGTGTCAGA GTTTTTAAGT ACAGGTGTAG TCATCCTCTG
 -3 A  Y  A  D   I  V  M   T  Q  S   Q  K  F  M   S  T  S   V  G  D

121 AGGGTCAGCG TCACCTGCAA GGCCAGTCAG AATGTGGGTA CTAATGTAGC CTGGTATCAA
    TCCCAGTCGC AGTGGACGTT CCGGTCAGTC TTACACCCAT GATTACATCG GACCATAGTT
 18 R  V  S  V   T  C  K   A  S  Q   N  V  G  T   N  V  A   W  Y  Q
                      *   *  *  *   *  *  *  *   *  *  *
                                     CDR #1

181 CAGAAACCAG GGCAATCTCC TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA
    GTCTTTGGTC CCGTTAGAGG ATTTCGTGAC TAAATGAGCA GTAGGATGGC CATGTCACCT
 38 Q  K  P  G   Q  S  P   K  A  L   I  Y  S  S   S  Y  R   Y  S  G
                                     *  *  *  *   *  *  *
                                              CDR #2

241 GTCCCTGATC GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT
    CAGGGACTAG CGAAGTGTCC GTCACCTAGA CCCTGTCTAA AGTGAGAGTG GTAGTCGGTA
 58 V  P  D  R   F  T  G   S  G  S   G  T  D  F   T  L  T   I  S  H

301 GTGCAGTCTG AAGACTTGGC AGACTATTTC TGTCAGCAAT ATAACATCTA TCCTCTCACG
    CACGTCAGAC TTCTGAACCG TCTGATAAAG ACAGTCGTTA TATTGTAGAT AGGAGAGTGC
 78 V  Q  S  E   D  L  A   D  Y  F   C  Q  Q  Y   N  I  Y   P  L  T
                                     *  *  *  *   *  *  *   *  *  *
                                              CDR #3

                                  BstBI
361 TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG CTGCACCATC TGTCTTCATC
    AAGCCAGGAC CCTGGTTCGA CCTCGAAGCT TCTCGACACC GACGTGGTAG ACAGAAGTAG
 98 F  G  P  G   T  K  L   E  L  R   R  A  V  A   A  P  S   V  F  I

421 TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCTT CTGTTGTGTG CCTGCTGAAT
    AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGAA GACAACACAC GGACGACTTA
118 F  P  P  S   D  E  Q   L  K  S   G  T  A  S   V  V  C   L  L  N

481 AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT
    TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA
138 N  F  Y  P   R  E  A   K  V  Q   W  K  V  D   N  A  L   Q  S  G

541 AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
    TTGAGGGTCC TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG
158 N  S  Q  E   S  V  T   E  Q  D   S  K  D  S   T  Y  S   L  S  S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC
    TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
178 T  L  T  L   S  K  A   D  Y  E   K  H  K  V   Y  A  C   E  V  T

661 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG
    GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC
198 H  Q  G  L   S  S  P   V  T  K   S  F  N  R   G  E  C  (SEQ ID NO.25)

711   TTAA  (SEQ ID NO.24)
      AATT
216    O
```

FIG. 19

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT TAGTGCCGCC TGGAGGGTCC
    CGCATGCGAC TCCACGTCGA CCACCTCAGA CCCCCTCCGA ATCACGGCGG ACCTCCCAGG
 -3 A  Y  A  E   V  Q  L   V  E  S   G  G  G  L   V  P  P   G  G  S

121 CTGAAACTCT CCTGTGCAGC CTCTGGATTC ATATTCAGTA GTTATGGCAT GTCTTGGGTT
    GACTTTGAGA GGACACGTCG GAGACCTAAG TATAAGTCAT CAATACCGTA CAGAACCCAA
 18 L  K  L  S   C  A  A   S  G  F   I  F  S  S   Y  G  M   S  W  V
                                                 *  *  *  *  *
                                          CDR #1

181 CGCCAGACTC CAGGCAAGAG CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC
    GCGGTCTGAG GTCCGTTCTC GGACCTCAAC CAGCGTTGGT AATTATTATT ACCACTATCG
 38 R  Q  T  P   G  K  S   L  E  L   V  A  T  I   N  N  N   G  D  S
                                       *  *  *  *  *  *  *  *

241 ACCTATTATC CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC
    TGGATAATAG GTCTGTCACA CTTCCCGGCT AAGTGGTAGA GGGCTCTGTT ACGGTTCTTG
 58 T  Y  Y  P   D  S  V   K  G  R   F  T  I  S   R  D  N   A  K  N
    *  *  *  *   *  *  *   *
          CDR #2

301 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT TTACTGTGCA
    TGGGACATGG ACGTTTACTC GTCAGACTTC AGACTCCTGT GTCGGTACAA AATGACACGT
 78 T  L  Y  L   Q  M  S   S  L  K   S  E  D  T   A  M  F   Y  C  A

361 AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTTACTGGG GCCAAGGGAC TCTGGTCACT
    TCTCGGGAGT AATCAAGCCG ATGAACCAAA CCAATGACCC CGGTTCCCTG AGACCAGTGA
 98 R  A  L  I   S  S  A   T  W  F   G  Y  W  G   Q  G  T   L  V  T
       *  *  *   *  *  *   *  *  *   *  *
                    CDR #3
                          ApaI
421 GTCTCTGCAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCCTC CTCCAAGAGC
    CAGAGACGTC GGAGGTGGTT CCCGGGTAGC CAGAAGGGGG ACCGTGGGAG GAGGTTCTCG
118 V  S  A  A   S  T  K   G  P  S   V  F  P  L   A  P  S   S  K  S

481 ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG
    TGGAGACCCC CGTGTCGCCG GGACCCGACG GACCAGTTCC TGATGAAGGG GCTTGGCCAC
138 T  S  G  G   T  A  A   L  G  C   L  V  K  D   Y  F  P   E  P  V

541 ACGGTGTCGT GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA
    TGCCACAGCA CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT
158 T  V  S  W   N  S  G   A  L  T   S  G  V  H   T  F  P   A  V  L

601 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
    GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCACTGGC ACGGGAGGTC GTCGAACCCG
178 Q  S  S  G   L  Y  S   L  S  S   V  V  T  V   P  S  S   S  L  G
```

FIG. 20A

```
661 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA
    TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT
198 T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K

721 GTTGAGCCCA AATCTTGTGA CAAAACTCAC ACATGA   (SEQ ID NO.26)
    CAACTCGGGT TTAGAACACT GTTTTGAGTG TGTACT
218 V  E  P  K  S  C  D  K  T  H  T  O        (SEQ ID NO.27)
```

FIG. 20B

Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACTGTTCAGGACGCC 3' (SEQ ID NO.1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3' (SEQ ID NO.2)

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3' (SEQ ID NO.3)

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3' (SEQ ID NO.4)

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3' (SEQ ID NO.5)

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3' (SEQ ID NO.6)

FIG. 21

Light chain forward primer

6G4.light.Nsi 36-MER

```
5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC  3' (SEQ ID NO.28)
                  T   T           T       T        (SEQ ID NO.29)
                                  A       A        (SEQ ID NO.30)
```

Light chain reverse primer

6G4.light.Mun 35-MER

```
5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3' (SEQ ID NO.31)
```

FIG. 22

Heavy chain forward primer

6G4.heavy.Mlu 32-MER

5' CAAACGCGTACGCT GAG ATC CAG CTG CAG CAG 3' (SEQ ID NO.32)
T C (SEQ ID NO.33)

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCGG ATAGACCGATGGGGCTGTTGTTTTGGC 3' (SEQ ID NO.11)
T (SEQ ID NO.15)
A (SEQ ID NO.14)
G (SEQ ID NO.13)

FIG. 23

```
 70 G ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
    C TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
 1  D   I  V  M   T  Q  T   P  L  S  L   P  V  S   L  G  D

121 CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT
    GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
 18 Q  A  S  I   S  C  R   S  S  Q   S  L  V  H   G  I  G   N  T  Y
                   *   *  *  *  *  *  *  *  *  *  *  *  *  *
                                      CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
    AATGTAACCA TGGACGTCTT CGGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
 38 L  H  W  Y   L  Q  K   P  G  Q   S  P  K  L   L  I  Y   K  V  S
    *  *                                                    *  *  *
                                                        CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA
    TTGGCTAAAA GACCCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
 58 N  R  F  S   G  V  P   D  R  F   S  G  S  G   S  G  T   D  F  T
    *  *  *  *
                                                        CDR #3

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
    GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
 78 L  R  I  S   R  V  E   A  E  D   L  G  L  Y   F  C  S   Q  S  T
                                                  *  *  *  *
                                                        CDR #3

361 CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGATGCTGCA
    GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCG ACTACGACGT
 98 H  V  P  L   T  F  G   A  G  T   K  L  E  L   K  R  A   D  A  A
    *  *  *  *   *
                                      MunI
421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA  (SEQ ID NO.34)
    GGTTGACATA GGTAGAAGGG TGGTAGGTCA CTCGTTAACT
118 P  T  V  S   I  F  P   P  S  S   E  Q  L  K  (SEQ ID NO.35)
```

FIG. 24

```
 70 G AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
    C TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
  1 E   I  Q  L   Q  Q  S   G  P  E  L   M  K  P   G  A  S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAGTA GCCACTACAT GCACTGGGTG
    CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
 18 V  K  I  S   C  K  A   S  G  Y  S  F  S  S  H  Y  M  H  W  V
                                                 *  *  *  *  *
                                          CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
    TTCGTCTCGG TACCTTTCTC GGAACTCACC TAACCGATGT AACTAGGAAG GTTACCACTT
 38 K  Q  S  H   G  K  S   L  E  W   I  G  Y  I   D  P  S  N  G  E
                                       *  *  *  *  *  *  *  *  *
                                                CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
    TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAACT GACATCTGTG TAGAAGGTCG
 58 T  T  Y  N   Q  K  F   K  G  K   A  T  L  T   V  D  T   S  S  S
    *  *  *  *   *  *  *   *  *
301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
    TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
 78 T  A  N  V   H  L  S   S  L  T   S  D  D  S   A  V  Y   F  C  A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
    TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
 98 R  G  D  Y   R  Y  N   G  D  W   F  F  D  V   W  G  A   G  T  T
       *  *  *   *  *  *   *  *  *   *  *  *  *
                      CDR #3

     BstEII                                                ApaI
421 GTCACCGTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGCC
    CAGTGGCAGA GGAGGCGGAT TTGGCTGTCG GGGTAGCCAG ATAGGCCCGG
118 V  T  V  S   S  A  K   T  D  S   P  I  G  L   S  G  P

471 CATC  (SEQ ID NO.36)
    GTAG
135  I    (SEQ ID NO.37)
```

FIG. 25

5' CTTGGTGGAGGCGGAGGAGACG 3' (SEQ ID NO.38)

Mutagenesis Primer for 6G425VL

DS/VF 38MER

5' GAAACGGGCTGTTGCTGCACCAACTGTATTCATCTTCC 3' (SEQ ID NO.39)

SYN.BstEII 31 MER

5' GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 3' (SEQ ID NO.40)

SYN.Apa 22 MER

5' CTTGGTGGAGGCGGAGGAGACG 3' (SEQ ID NO.38)

FIG. 26

```
  1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT
    TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA
-23 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N

 61 GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
    CGTATGCGAC TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
 -3 A  Y  A  D   I  V  M   T  Q  T   P  L  S  L   P  V  S   L  G  D

121 CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT
    GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
 18 Q  A  S  I   S  C  R   S  S  Q   S  L  V  H   G  I  G   N  T  Y
                     *      *  *  *   *  *  *  *   *  *  *   *  *  *
                                        CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
    AATGTAACCA TGGACGTCTT CGGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
 38 L  H  W  Y   L  Q  K   P  G  Q   S  P  K  L   L  I  Y   K  V  S
    *  *                                                     *  *  *
                                                            CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA
    TTGGCTAAAA GACCCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
 58 N  R  F  S   G  V  P   D  R  F   S  G  S  G   S  G  T   D  F  T
    *  *  *  *
301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
    GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
 78 L  R  I  S   R  V  E   A  E  D   L  G  L  Y   F  C  S   Q  S  T
                                                    *  *  *  *
                                                    CDR #3

361 CATGTTCCGC TCACGTTCGG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGTTGCTGCA
    GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCG ACAACGACGT
 98 H  V  P  L   T  F  G   A  G  T   K  L  E  L   K  R  A   V  A  A
    *  *  *  *   *

421 CCAACTGTAT TCATCTTCCC ACCATCCAGT GAGCAATTGA AATCTGGAAC TGCCTCTGTT
    GGTTGACATA AGTAGAAGGG TGGTAGGTCA CTCGTTAACT TTAGACCTTG ACGGAGACAA
118 P  T  V  F   I  F  P   P  S  S   E  Q  L  K   S  G  T   A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L   N  N  F   Y  P  R   E  A  K  V   Q  W  K   V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S   G  N  S   Q  E  S   V  T  E  Q   D  S  K   D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S   S  T  L   T  L  S   K  A  D  Y   E  K  H   K  V  Y
```

FIG. 27A

```
661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R  G

721 GAGTGTTAA  (SEQ ID NO.41)
    CTCACAATT
218 E  C  O    (SEQ ID NO.42)
```

FIG. 27B

```
   1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
     TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23  M  K  K  N     I  A  F     L  L  A     S  M  F  V     F  S  I     A  T  N

  61 GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
     CGCATGCGAC TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
 -3  A  Y  A  E     I  Q  L     Q  Q  S     G  P  E  L     M  K  P     G  A  S

 121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAGTA GCCACTACAT GCACTGGGTG
     CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
  18  V  K  I  S     C  K  A     S  G  Y     S  F  S  S     H  Y  M     H  W  V
                                                *  *  *  *     *
                                                      CDR #1

 181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
     TTCGTCTCGG TACCTTTCTC GGAACTCACC TAACCGATGT AACTAGGAAG GTTACCACTT
  38  K  Q  S  H     G  K  S     L  E  W     I  G  Y  I     D  P  S     N  G  E
                                                *  *     *  *  *     *  *  *
                                                            CDR #2

 241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
     TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAACT GACATCTGTG TAGAAGGTCG
  58  T  T  Y  N     Q  K  F     K  G  K     A  T  L  T     V  D  T     S  S  S
      *  *  *  *     *  *  *     *  *

 301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
     TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
  78  T  A  N  V     H  L  S     S  L  T     S  D  D  S     A  V  Y     F  C  A

 361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
     TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
  98  R  G  D  Y     R  Y  N     G  D  W     F  F  D  V     W  G  A     G  T  T
         *  *  *     *  *  *     *  *  *     *  *  *  *
                        CDR #3

 421 GTCACCGTCT CCTCCGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
     CAGTGGCAGA GGAGGCGGAG GTGGTTCCCG GGTAGCCAGA AGGGGGACCG TGGGAGGAGG
 118  V  T  V  S     S  A  S     T  K  G     P  S  V  F     P  L  A     P  S  S

 481 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA
     TTCTCGTGGA GACCCCCGTG TCGCCGGGAC CCGACGGACC AGTTCCTGAT GAAGGGGCTT
 138  K  S  T  S     G  G  T     A  A  L     G  C  L  V     K  D  Y     F  P  E

 541 CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT
     GGCCACTGCC ACAGCACCTT GAGTCCGCGG GACTGGTCGC CGCACGTGTG GAAGGGCCGA
 158  P  V  T  V     S  W  N     S  G  A     L  T  S  G     V  H  T     F  P  A

 601 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC
     CAGGATGTCA GGAGTCCTGA GATGAGGGAG TCGTCGCACC ACTGGCACGG GAGGTCGTCG
 178  V  L  Q  S     S  G  L     Y  S  L     S  S  V  V     T  V  P     S  S  S
```

FIG. 28A

```
661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC
    AACCCGTGGG TCTGGATGTA GACGTTGCAC TTAGTGTTCG GGTCGTTGTG GTTCCACCTG
198 L  G  T  Q   T  Y  I   C  N  V   N  H  K  P   S  N  T   K  V  D

721 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GA  (SEQ ID NO.43)
    TTCTTTCAAC TCGGGTTTAG AACACTGTTT TGAGTGTGTA CT
218 K  K  V  E   P  K  S   C  D  K   T  H  T  O     (SEQ ID NO.44)
```

FIG. 28B

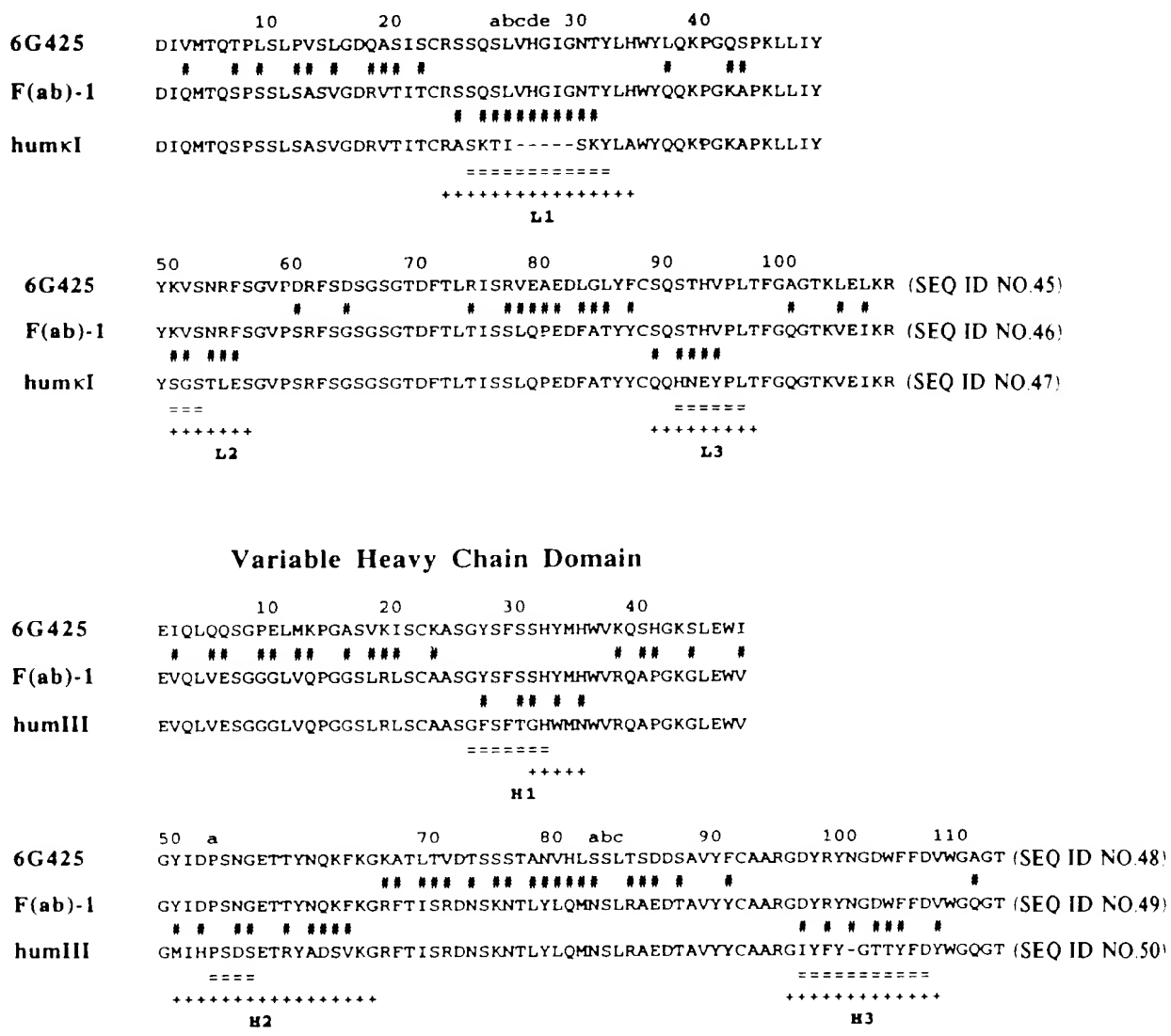


FIG. 29

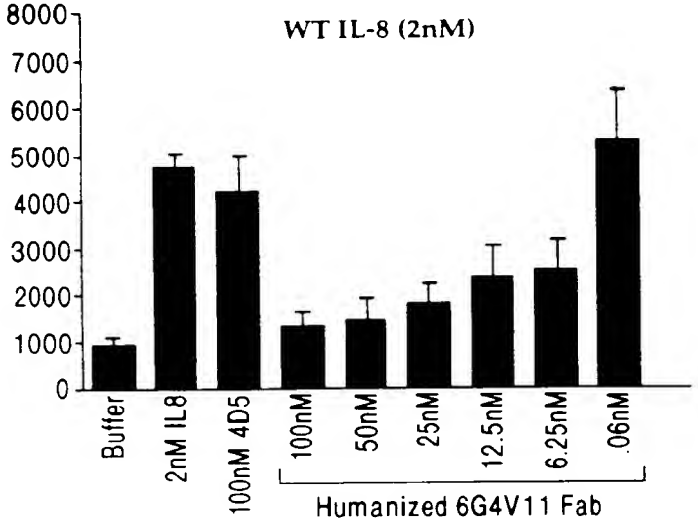


FIG. 30A

IC50~12nM

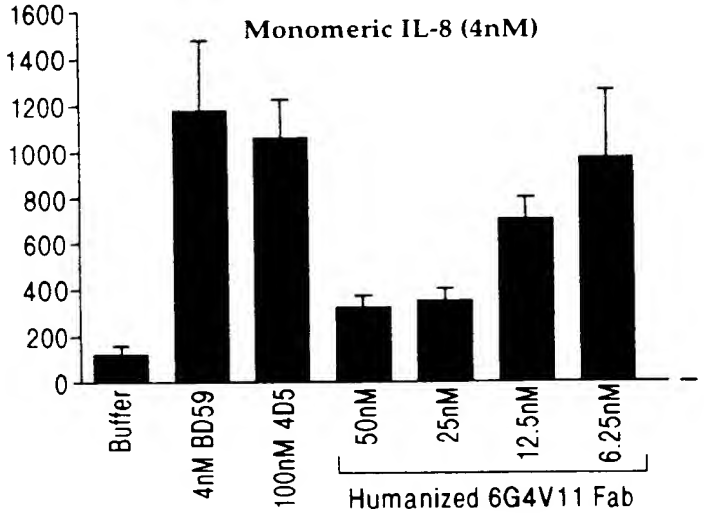


FIG. 30B

IC50~15nM

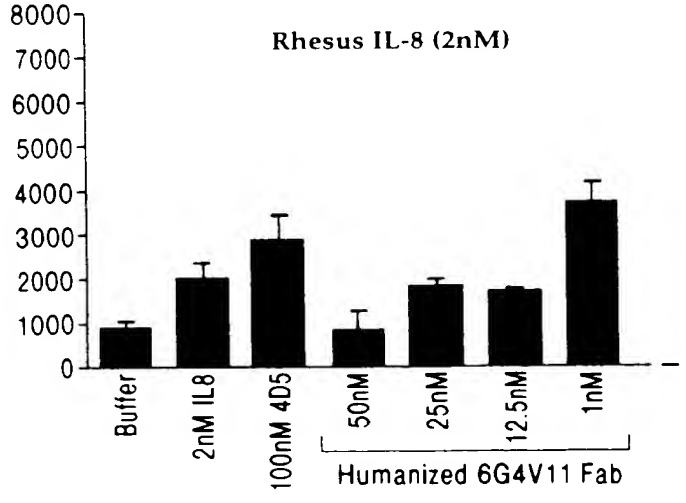


FIG. 30C

IC50~22nM

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO.51)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLV**Q**SGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFT**L**SRDNSKNT**A**YLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO.52)

Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)

SGGGSGSGDFDYEKMANANKGAMTENADENALQSDAKGKLDSVATDYGAAIDGFIGDVS
GLANGNGATGDFAGSSNSQMAQVGDGDNSPLMNNFRQYLPSLPQSVECRPFVFSAGKPY
EFSIDCDKINLFRGVFAFLLYVATFMYVFSTFANILRNKES (SEQ ID NO.53)

FIG. 31A

```
   1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
     TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
 -23 M  K  K  N    I  A  F    L  L  A    S  M  F  V    F  S  I    A  T  N

  61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
     CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
  -3 A  Y  A  D    I  Q  M    T  Q  S    P  S  S  L    S  A  S    V  G  D

 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACACGTAT
     TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
  18 R  V  T  I    T  C  R    S  S  Q    S  L  V  H    G  I  G    N  T  Y

 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
     AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
  38 L  H  W  Y    Q  Q  K    P  G  K    A  P  K  L    L  I  Y    K  V  S

 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
     TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
  58 N  R  F  S    G  V  P    S  R  F    S  G  S  G    S  G  T    D  F  T

 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
     GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
  78 L  T  I  S    S  L  Q    P  E  D    F  A  T  Y    Y  C  S    Q  S  T

 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
     GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
  98 H  V  P  L    T  F  G    Q  G  T    K  V  E  I    K  R  T    V  A  A

 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
     GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
 118 P  S  V  F    I  F  P    P  S  D    E  Q  L  K    S  G  T    A  S  V

 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
     CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
 138 V  C  L  L    N  N  F    Y  P  R    E  A  K  V    Q  W  K    V  D  N

 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
     CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
 158 A  L  Q  S    G  N  S    Q  E  S    V  T  E  Q    D  S  K    D  S  T

 601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
     ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
 178 Y  S  L  S    S  T  L    T  L  S    K  A  D  Y    E  K  H    K  V  Y

 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
     CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
 198 A  C  E  V    T  H  Q    G  L  S    S  P  V  T    K  S  F    N  R  G

                                                                    (SEQ ID NO:54)
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
     CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
 218 E  C  O (SEQ ID NO:51)
```

FIG. 31B

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO.51)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVKQ**A**PGKGLEWVGYIDPSNGETTYNQKFKGRFT**L**SRDNSKNT**A**YLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO.55)

FIG. 31C

FIG. 32

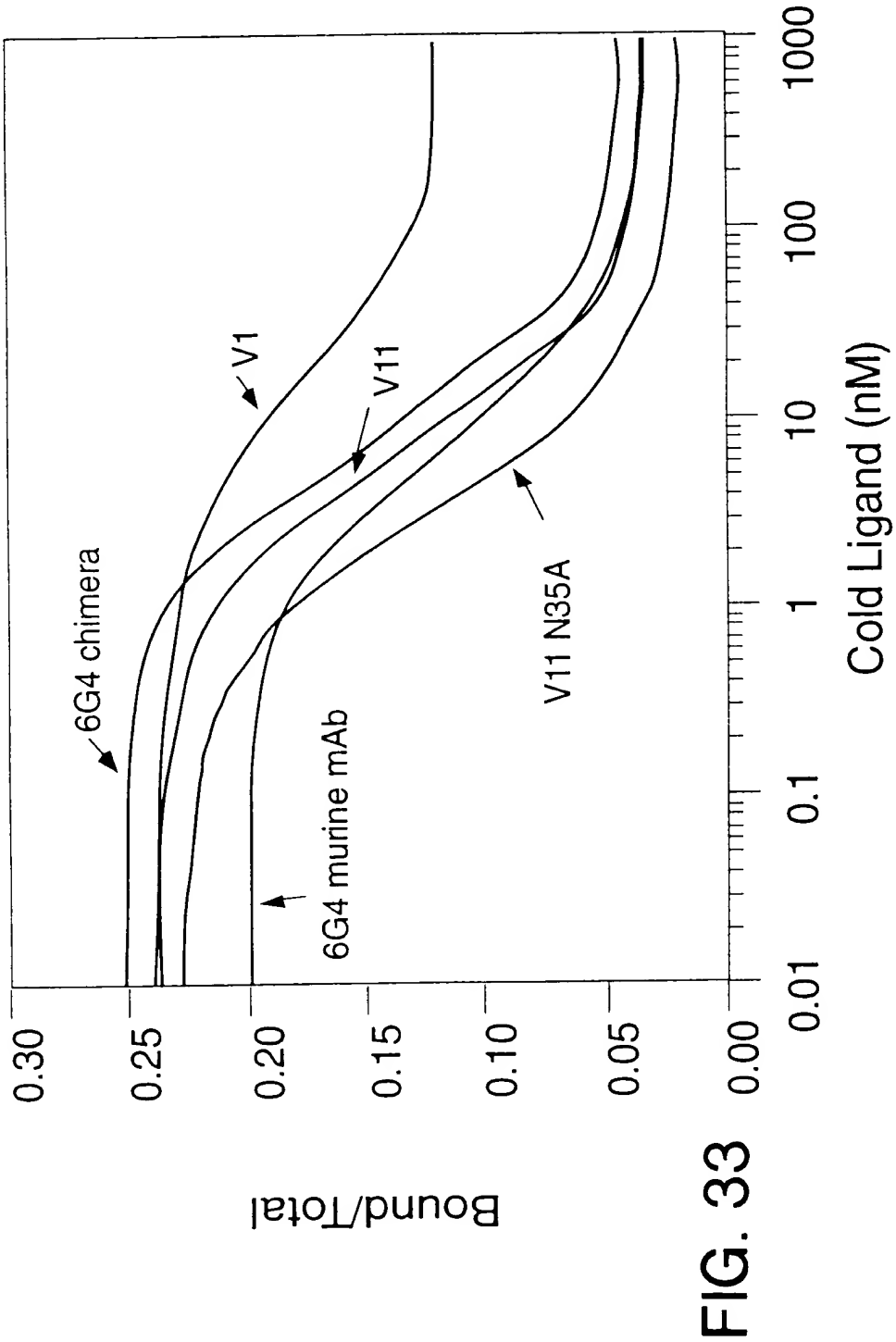


FIG. 33

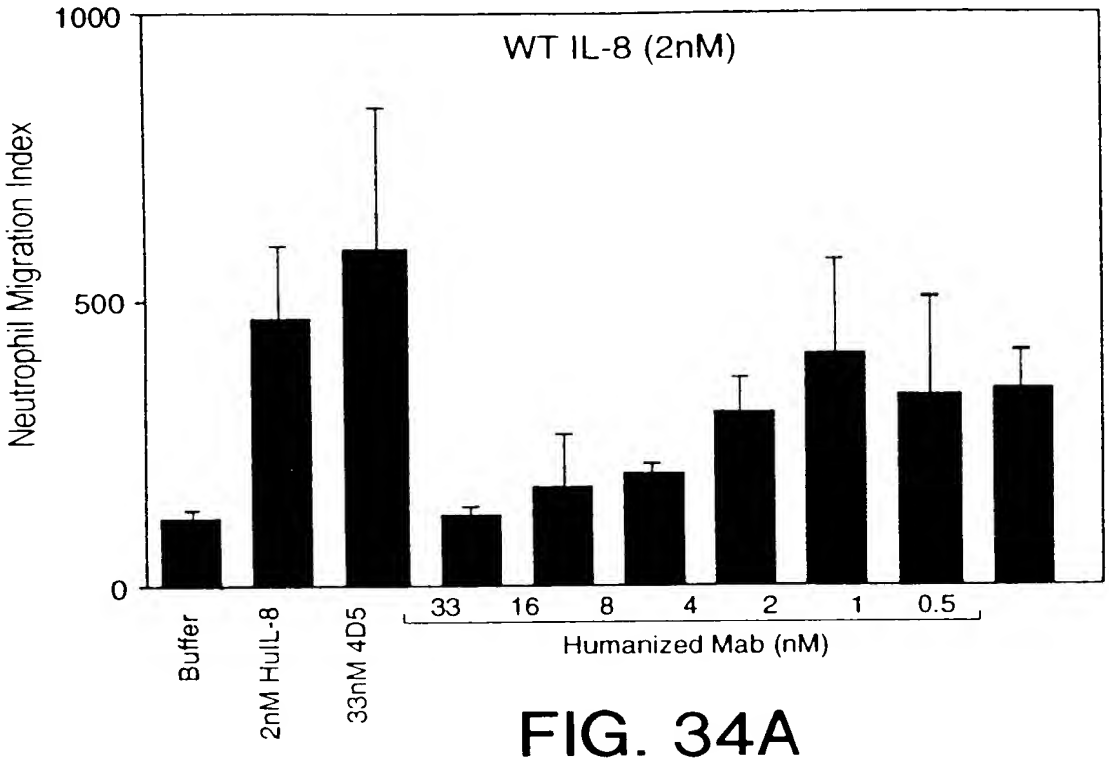


FIG. 34A

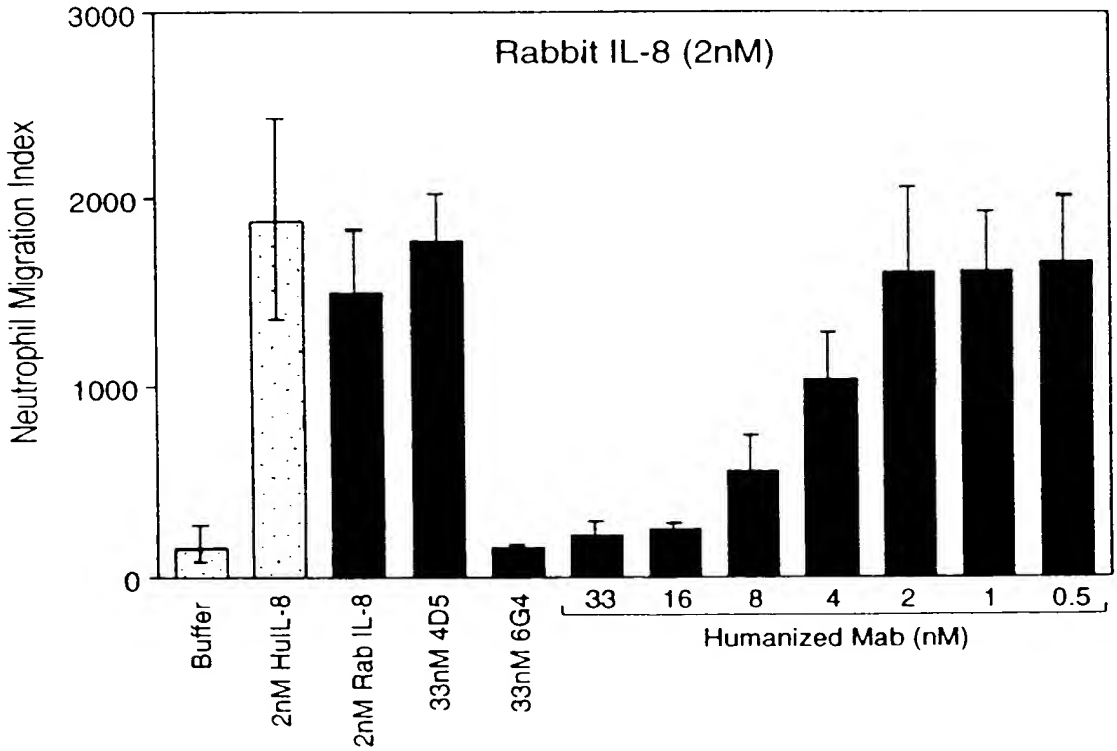


FIG. 34B

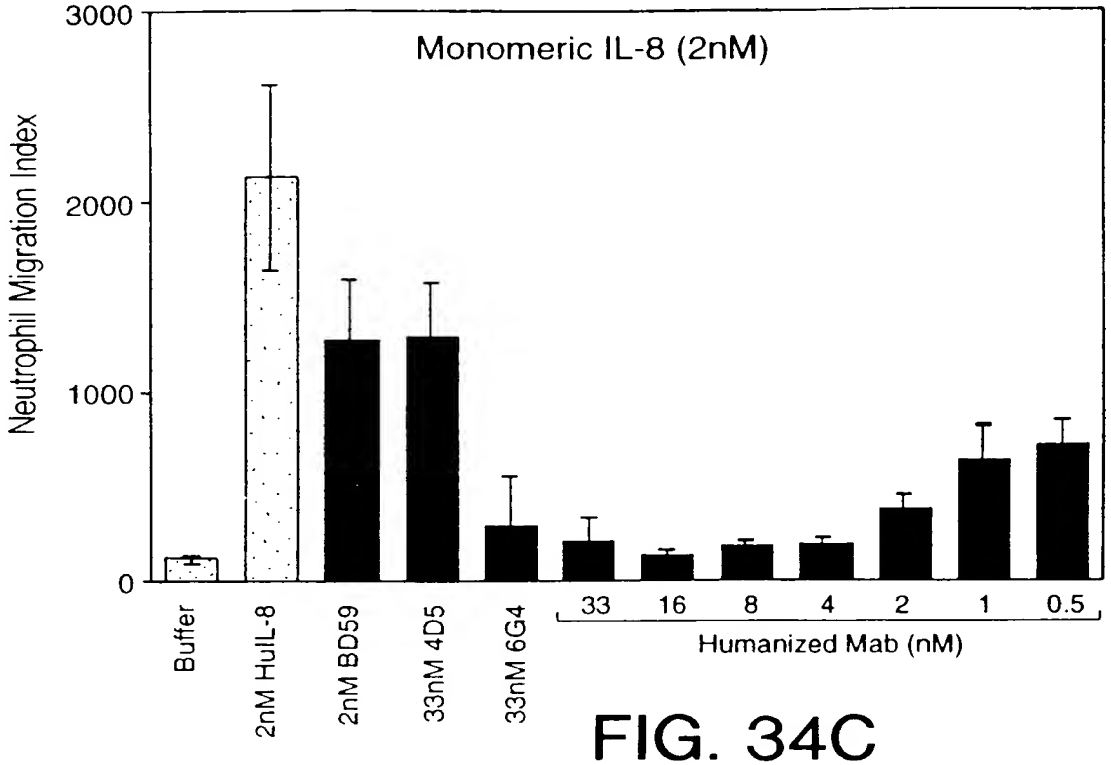


FIG. 34C

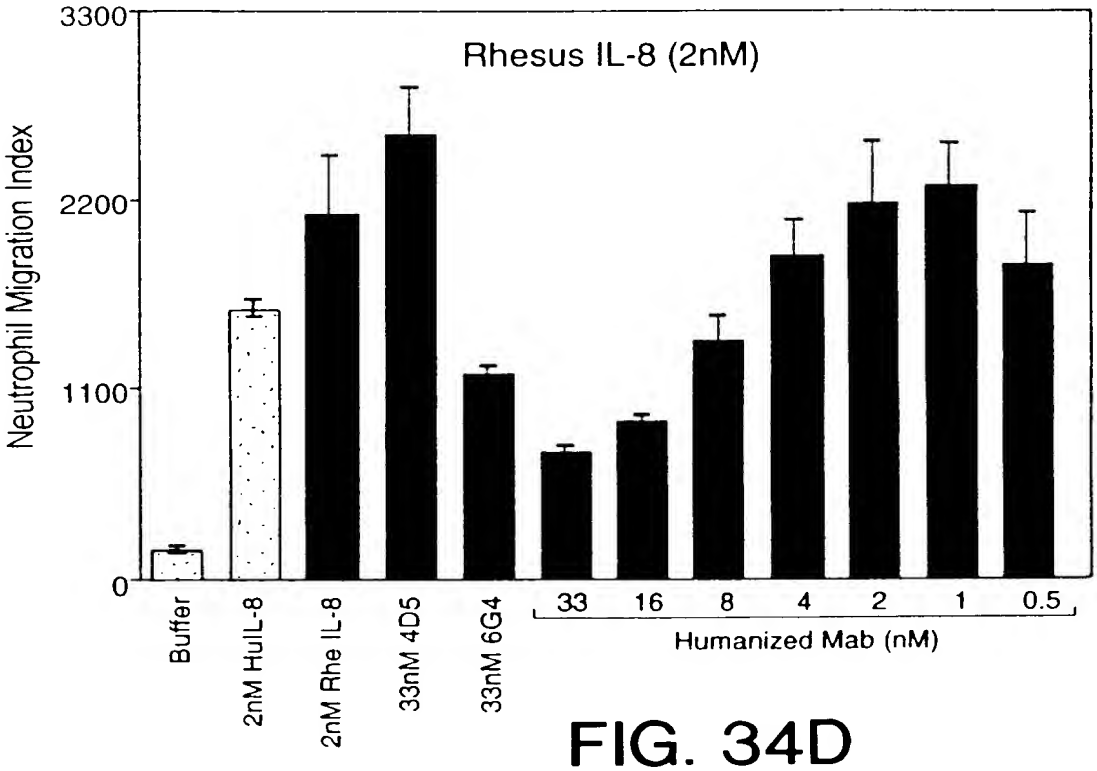


FIG. 34D

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIG**A**TY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC (SEQ ID NO.56)

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT (SEQ ID NO.52)

Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper

CPPCPAPE<u>LL</u>GGRMKQLEDKVEELLSKNYHLENEVARLKKLVGER (SEQ ID NO.57)

FIG. 35

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N    I  A  F    L  L  A    S  M  F  V    F  S  I    A  T  N

 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
    CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A  Y  A  D    I  Q  M    T  Q  S    P  S  S  L    S  A  S    V  G  D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT
    TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
 18 R  V  T  I    T  C  R  S  S  Q    S  L  V  H    G  I  G    A  T  Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
    AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L  H  W  Y    Q  Q  K    P  G  K    A  P  K  L    L  I  Y    K  V  S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
    TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N  R  F  S    G  V  P    S  R  F    S  G  S  G    S  G  T    D  F  T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
    GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L  T  I  S    S  L  Q    P  E  D    F  A  T  Y    Y  C  S    Q  S  T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
    GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H  V  P  L    T  F  G    Q  G  T    K  V  E  I    K  R  T    V  A  A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
    GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P  S  V  F    I  F  P    P  S  D    E  Q  L  K    S  G  T    A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L    N  N  F    Y  P  R    E  A  K  V    Q  W  K    V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S    G  N  S    Q  E  S    V  T  E  Q    D  S  K    D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S    S  T  L    T  L  S    K  A  D  Y    E  K  H    K  V  Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V    T  H  Q    G  L  S    S  P  V  T    K  S  F    N  R  G
                                                                (SEQ ID NO.58)
721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
    CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E  C  O (SEQ ID NO.56)
```

FIG. 36

```
781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
    TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT
 -1                                   M  K  K  N     I  A  F     L  L  A

841 TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT
    AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S  M  F  V     F  S  I     A  T  N     A  Y  A  E     V  Q  L     V  Q  S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
    CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
 8  G  G  G  L     V  Q  P     G  G  S     L  R  L  S     C  A  A     S  G  Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
    AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
 28 S  F  S  S     H  Y  M     H  W  V     R  Q  A  P     G  K  G     L  E  W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
     CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
 48  V  G  Y  I     D  P  S     N  G  E     T  T  Y  N     Q  K  F     K  G  R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
     AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
 68  F  T  L  S     R  D  N     S  K  N     T  A  Y  L     Q  M  N     S  L  R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
     CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
 88  A  E  D  T     A  V  Y     Y  C  A     R  G  D  Y     R  Y  N     G  D  W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
     AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
 108 F  F  D  V     W  G  Q     G  T  L     V  T  V  S     S  A  S     T  K  G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
     GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCCGTG TCGCCGGGAC
 128 P  S  V  F     P  L  A     P  S  S     K  S  T  S     G  G  T     A  A  L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
     CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
 148 G  C  L  V     K  D  Y     F  P  E     P  V  T  V     S  W  N     S  G  A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
     GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
 168 L  T  S  G     V  H  T     F  P  A     V  L  Q  S     S  G  L     Y  S  L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
     TCGTCGCACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
 188 S  S  V  V     T  V  P     S  S  S     L  G  T  Q     T  Y  I     C  N  V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
     TTAGTGTTCG GGTCGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
 208 N  H  K  P     S  N  T     K  V  D     K  K  V  E     P  K  S     C  D  K

1561 ACTCACACAT GCCCGCCGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA
     TGAGTGTGTA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTCGAT
 228 T  H  T  C     P  P  C     P  A  P     E  L  L  G     G  R  M     K  Q  L
```

FIG. 37A

```
1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA
     CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT
 248 E  D  K  V   E  E  L   L  S  K   N  Y  H  L   E  N  E   V  A  R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA   (SEQ ID NO.59)
     GAGTTTTTCG AACAGCCCCT CGCGATT
 268 L  K  K  L   V  G  E   R  O     (SEQ ID NO.60)
```

FIG. 37B

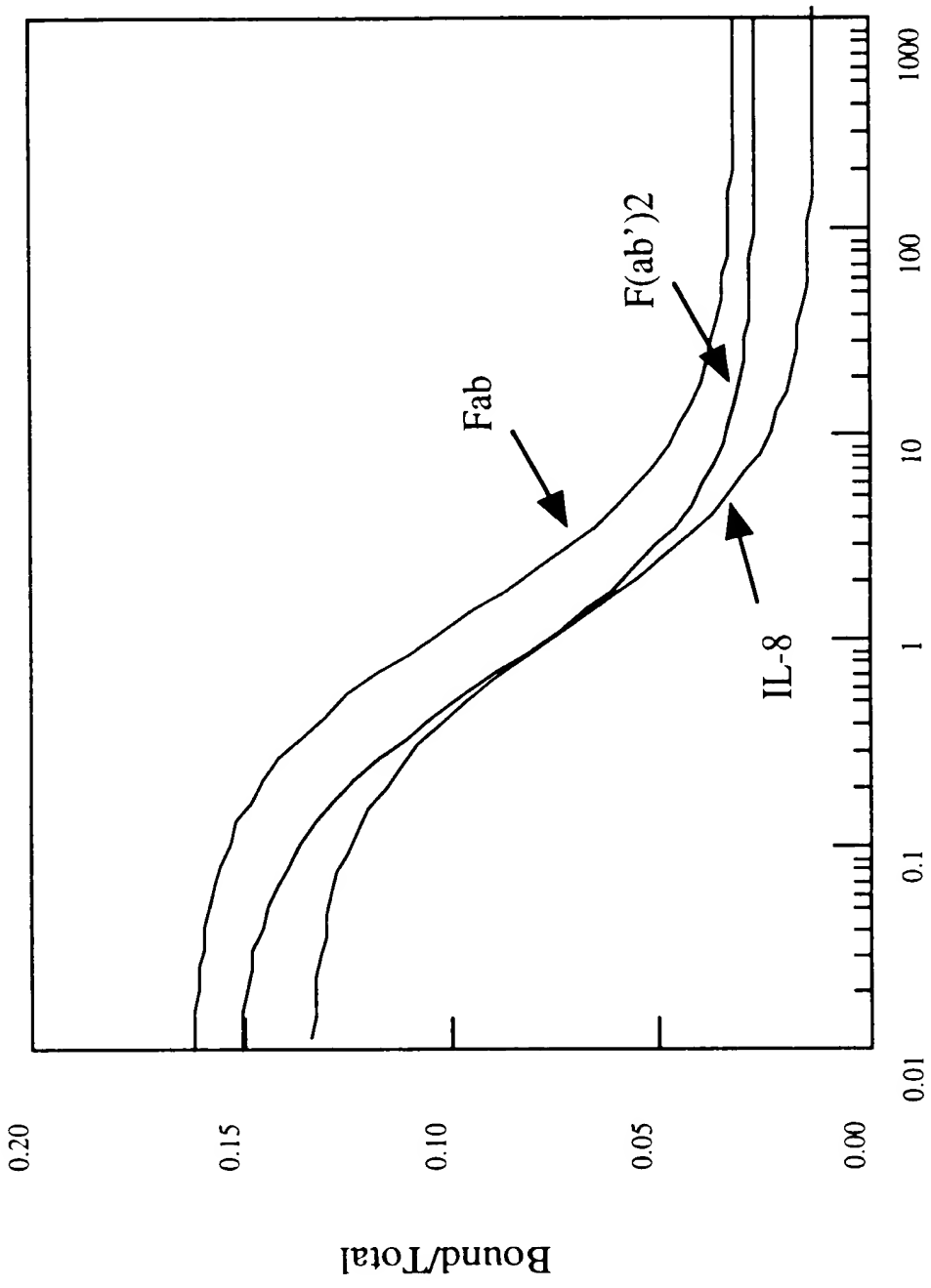


FIG. 38

FIG. 39

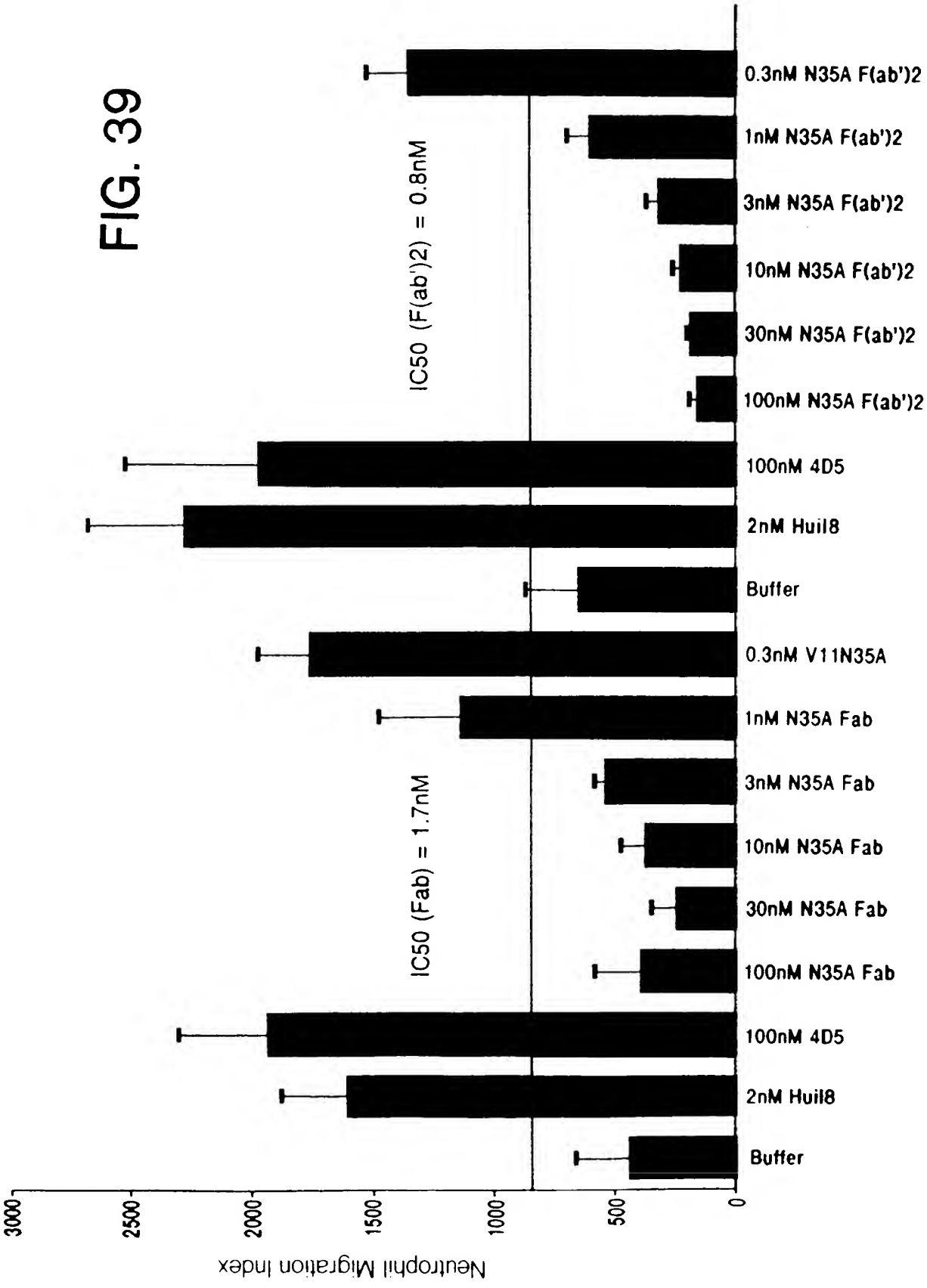
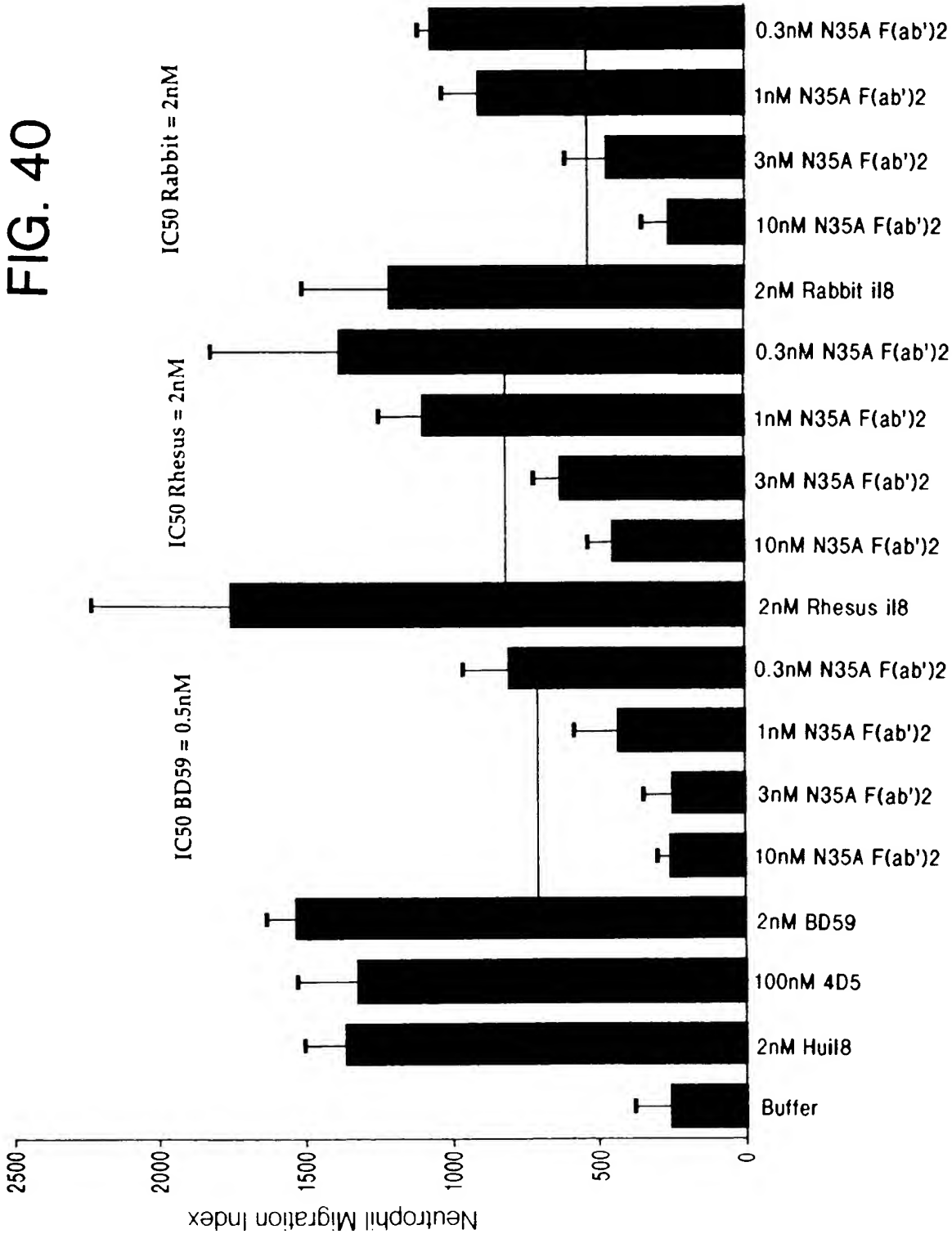


FIG. 40



```
                                                                                 aluI                 pleI
                                                                                 hindIII            mboII  taqI
    ecoRI       pflMI                                               ddeI        tru9I               earI/ksp632I
    apoI        bslI                                  nlaIII     bsrDI          mseI cac8I       mboII  hinfI
  1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

              bspMI                                                                                 sau3AI
           hinPI                                                                                    mboI/ndeII[dam-]
           hhaI/cfoI                                                                                dpnI[dam+]
          mstI         aluI              mslI                    hinPI           aciI               dpnII[dam-]
          aviII/fspI  hindIII          maeIII bsrDI              hhaI/cfoI      nspBII             bclI[dam-] mnlI
101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

                                                                thaI
                                                                fnuDII/mvnI
                                                             fnu4HI
                                                             bsoFI
                                                             bbvI       maeII
       rsaI                                                fnu4HI bstUI snaBI
     hinPI                                                 bsoFI  bsh1236I
     hhaI/cfoI mnlI                cac8I                   bbvI  hinPI    bsaAI                    mnlI
    haeII csp6I                 sfaNI   bsmI              aluI   hhaI/cfoI                       fokI
                                                                                                 sfaNI
201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

                                                                                                          aluI
                                                                                                          sstI
                                                                                                          sacI
                                                                                                          hgiJII
                                          haeIII/palI                                                     hgiAI/aspHI
                                         mcrI                                                             ecl136II
                                         eagI/xmaIII/eclXI                                          ecoRI bsp1286
                                         eaeI                                                   rmaI      bsiHKAI
                     aluI                cfrI                                                   maeI      bmyI
        tru9I       pvuII                bsiEI  ahdI/eam1105I                  tru9I            bfaI    taqI
        mseI        nspBII           maeIII   bsmAI                             mseI         maeIII  apoI  banII
301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CTTAAGCTCG
```

FIG. 41A

```
          scrFI
          nciI
          mspI
          hpaII
          dsaV
         xmaI/pspAI
         smaI
         scrFI
         nciI
         dsaV
         cauII        xhoI
         bsaJI     mnlI
         avaI   sau3AI taqI
       rsaI      mboI/ndeII[dam-]
       csp6I     dpnI[dam+]
      nlaIV     nlaIV  paeR7I
      kpnI cauII dpnII[dam-]
      hgiCI     bstYI/xhoII
      banI bsaJI alwI[dam-]
      asp718    bamHI  avaI        hphI
      acc65I    alwI[dam-] mnlI  mnlI                                  mboII   sfaNI
401 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG CTACAAACGC
    AGCCATGGGC CCCTAGGAGA GCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC GATGTTTGCG
-23                                      M   K   K   N   I   A   F   L   L   A   S   M   F   V   F   S   I   A   T   N   A
      a mutation was found that inactivated the mluI site.  The penultimate nucleotide was changed fr G toT ^

                                    sstI
                                    sacI
                                    hgiJII
                                    hgiAI/aspHI
                                    ecl136II                                                  bspMI
                                    bsp1286                                                 scfI
                                    bsiHKAI                                                 pstI
                               bsmFI  bmyI                                        hphI      sse8387I             ddeI   nlaIII
                            bsrI  avaI aluI          mnlI                      maeIII    bspMI                aluI   rsaI
          ecoRV       tth111I/aspI  banII       aciI                        bstEII  hphI bsgI              hindIII csp6I
501 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG TGGGCGATAG GGTCACCATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT
    TATGCGACTA TAGGTCTACT GGGTCAGGGG CTCGAGGGAC AGGCGGAGAC ACCCGCTATC CCAGTGGTAG TGGACGTCCA GTTCAGTTTC GAATCATGTA
 -2  Y   A   D   I   Q   M   T   Q   S   P   S   S   L   S   A   S   V   G   D   R   V   T   I   T   C   R   S   S   Q   S   L   V   H
```

FIG. 41B

```
                                                 scrFI
                                                 mvaI
                                                 ecoRII                                          tfiI
                                                 dsaV                                     hinfI        bsmFI
                                                 bstNI    aluI                          taqI    bpmI/gsuI[dcm-]
                                  bsrI           apyI[dcm+]                                 claI/bsp106   pleI
                                                                                            bspDI[dam-]   hinfI
601 GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT
    CCATATCCAC GATGCATAAA TGTGACCATA GTTGTCTTTG GTCCTTTTCG AGGCTTTGAT GACTAAATGT TTCATAGGTT AGCTAAGAGA CCTCAGGGAA
32  G  I  G  A  T  Y  L  H  W  Y  Q  Q  K  P  G  K  A  P  K  L  L  I  Y  K  V  S  N  R  F  S  G  V  P  S

                mspI
                hpaII
                bslI
               bsaWI
              sau3AI
              mboI/ndeII[dam-]
              dpnI[dam+]
              dpnII[dam-]                                   fnu4HI
              alwI[dam-]                                    bsoFI
             nlaIV                                          bbvI
             bstYI/xhoII                                  scfI       mboII                           rsaI
             bamHI                                        pstI       bpuAI                           csp6I
             alwI[dam-]   bsmFI                           bsgI       bbsI                            scaI  nlaIII
701 CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTCAC AGAGTACTCA
    GAGCGAAGAG ACCTAGGCCA AGACCCTGCC TAAAGTGAGA CTGGTAGTCG TCAGACGTCG GTCTTCTGAA GCGTTGAATA ATGACAAGTG TCTCATGAGT
66   R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  S  Q  S  T  H

                              styI
                              bsaJI
                            rsaI
                            csp6I
                           nlaIV
                           kpnI
                           hgiCI        sau3AI
      bsrBI                banI         mboI/ndeII[dam-]  fnu4HI       mboII
      aciI                 asp718       dpnI[dam+]        bsoFI       bpuAI         aciI
    bsmFI     maeII        acc65I       dpnII[dam-]       bbvI        bbsI     mboII
801 TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
    ACAGGGCGAG TGCAAACCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT
99  V  P  L  T  F  G  Q  G  T  K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K
```

FIG. 41C

```
                                                                                                   scrFI
                                                                                                   mvaI
                                                                                                   ecoRII
                                                                                                   dsaV
                                                  haeIII/palI                                      bstNI
      xmnI                 xmnI                 haeI      rsaI                     mnlI           bsaJI
      asp700          cac8I asp700             mnlI       csp6I                    bslI      maeIII apyI[dcm+]
 901 TCTGGAACTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
     AGACCTTGAC GAAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG
 132 S  G  T  A   S  V  V   C  L  L   N  N  F  Y   P  R  E   A  K  V   Q  W  K  V   D  N  A   L  Q  S   G  N  S  Q

                                                 fnu4HI
                                                 bsoFI          celII/espI
                                              ddeI              blpI/bpu1102I
         maeIII                           scfI  mnlI bbvI    hgaI ddeI                                accI   cac8I
1001 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
     TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG
 166  E  S  V   T  E  Q   D  S  K  D   S  T  Y   S  L  S   S  T  L  T   L  S  K   A  D  Y   E  K  H  K   V  Y  A

                      cac8I
                     aluI
                    sstI
                    sacI
                    hgiJII
                    hgiAI/aspHI
                    ecl136II
                    bsp1286
                    bsiHKAI
                    bmyI                                                            mnlI                       rmaI
               haeIII/palI                                                       sau3AI                        maeI
              sau96I banII                                                       mboI/ndeII[dam-]              bfaI
              asuI ddeI                                                     aluI dpnI[dam+]      hgaI        sau96I
      hphI     eco0109I/draII                                            tru9I   dpnII[dam-] mspI             haeIII/palI
     maeIII   alwNI[dcm-]        maeIII    aluI                         mseI    alwI[dam-]  hpaII sfaNI     asuI
1101 CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT
     GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT TGTCCCCTCT CACAATTCGA CTAGGAGATG CGGCCTGCGT AGCACCGGGA
 199  C  E  V   T  H  Q  G   L  S  S   P  V  T   K  S  F  N   R  G  E   C  O (SEQ ID NO.56)
```

FIG. 41D

```
             rmaI                           rmaI
             maeI                           maeI
        rsaI bfaI                           bfaI          hphI
        csp6I speI                          xbaI mnlI    mnlI                                          mboII    sfaNI
1201 AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT TTTTCTATTG
     TCATGCGTTG ATCAGCATTT TTCCCATAGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC
-23                                                          M  K  K  N   I  A  F  L   L  A  S   M  F  V   F  S  I  A

                                                                            scrFI
                                                                            mvaI
                                                                            ecoRII
                                                                            dsaV
               rsaI                                              scrFI
              bsiWI/splI                                         mvaI   fnu4HI
             thaI                                                ecoRII
             fnuDII/mvnI                                         dsaV bstNI hgiJII                  aluI
             bstUI                   rmaI                        bstNI  bsoFI    bsp1286               alwNI[dcm-]
             bsh1236I                maeI                        apyI[dcm+] bsaJI bmyI                fnu4HI
            mluI csp6I  mnlI         bfaI                      haeIII/palI apyI[dcm+]                 bsoFI
            aflIII    ddeI         aluI           aciI haeI        bbvI     banII                     bbvI
1301 CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC
     GATGTTTGCG CATGCGACTC CAAGTCGATC ACGTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA GACCGATGAG
-5     T  N  A   Y  A  E   V  Q  L  V   Q  S  G   G  G  L   V  Q  P  G   G  S  L   R  L  S   C  A  A  S   G  Y  S

                                                 scrFI
                                                 nciI
                                                 mspI
                                                 hpaII
                                                 dsaV
                                                 cauII
                                                 bslI
                                                xmaI/pspAI
                                                smaI
                                                scrFI
                                                nciI
                                                dsaV        scrFI
                                                cauII       mvaI
                                                bslI        ecoRII
```

FIG. 41E

```
                                 bsaJI          dsaV
                                 avaI           bstNI
         pleI                   bsaJI           bslI                      bslI
         hinfI          sau96I sau96I           apyI[dcm+]               sau3AI
        taqI            avaII  nlaIV           sau96I               mboI/ndeII[dam-]
       xhoI             asuI   haeIII/palI     asuI                      dpnI[dam+]              maeII
       paeR7I          nlaIV   asuI           eco0109I/draII        dpnII[dam-]           snaBI
       avaI maeIII    bsrI    eco0109I/draII haeIII/palI                 alwI[dam-]    hphI     bsaAI
1401 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT
     GAAGAGCTCA GTGATATACG TGACCCAGGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCTATATAA CTAGGAAGGT TACCACTTTG ATGCATATTA
  29  F  S  S   H  Y  M  H   W  V  R   Q  A  P   G  K  G  L   E  W  V   G  Y  I   D  P  S  N   G  E  T   T  Y  N

                               thaI
                               fnuDII/mvnI            scfI
             haeIII/palI       bstUI                  pstI
            sau96I             bsh1236I               bsgI           cac8I   mnlI
            asuI              nruI                   bspMI         cac8I   ddeI  drdI
1501 CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT
     GTTTTCAAGT TCCCGGCAAA GTGAAATAGA GCGCTGTTGA GGTTTTTGTG TCGTATGGAC GTCTACTTGT CGGACGCACG ACTCCTGTGA CGGCAGATAA
  62 Q  K  F  K   G  R  F   T  L  S   R  D  N  S   K  N  T   A  Y  L   Q  M  N  S   L  R  A   E  D  T   A  V  Y  Y

                                                                                                   sau96I
                                                                                                   haeIII/palI
                                                                                                  sau96I
                                                                                                  nlaIV
                                                                                                  hgiJII
                                                                        maeIII                    bsp1286
                                                                       bstEII                     bsp120I
                                                                     scrFI                    bmyI
                                                                     mvaI          mnlI            banII
                                              maeII                  ecoRII   bsaJI           asuI
                                             hinlI/acyI              dsaV    bseRI            apaI
                                             ahaII/bsaHI             bstNI     esp3I           styI asuI
                                maeIII      taqI                    bsaJI hphI bsmBI      mnlI   bsaJI
           mnlI                hphI bsrI  mboII aatII          nlaIV apyI[dcm+] bsmAI   haeIII/palI eco0109I/draII
1601 ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTCGACGTC TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC
     TGACACGTTC TCCCCTAATA GCGATGTTAC CACTGACCAA GAAGCTGCAG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGGAGGT GGTTCCCGGG
  96  C  A  R   G  D  Y   R  Y  N  G   D  W  F   F  D  V   W  G  Q  G   T  L  V   T  V  S   S  A  S  T   K  G  P
                                                             seq right is from p6G425chim2.fab2   ^
```

FIG. 41F

```
                                                                                 scrFI
                                                                                 mvaI
                                                                       scrFI
                                                                       mvaI      ecoRII
                     nlaIV                                             ecoRII
                     hgiCI                                             dsaV
                     banI                                              bstNI     ecoNI
                  scrFI                                        sau96I dsaV
                  mvaI                                               haeIII/palI  bstNI                          hphI
                  ecoRII                                     fnu4HI     fnu4HI                         mspI
                  dsaV          hgiAI/aspHI                  bsoFI bsaJI     bslI                       hpaII
        mboII     bstNI     bseRI     bsp1286                      aciI  apyI[dcm+]                          cfr10I/bsrFI
       bpuAI      apyI[dcm+]  mnlI    bsiHKAI               bsp1286   asuI     bsoFI                         bsaWI  tth111I/aspI
       bbsI      bsaJI     mnlI       bmyI mnlI             bmyI nspBII bsaJI bbvI apyI[dcm+]          bslI  ageI maeIII
1701 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG
     TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTCGTGGAGA CCCCCGTGTC GCCGGGACCC GACGGACCAG TTCCTGATGA AGGGGCTTGG CCACTGCCAC
 129  S  V  F   P  L  A  P   S  S  K   S  T  S   G  G  T  A   A  L  G   C  L  V   K  D  Y  F   P  E  P   V  T  V

                 hinPI
                 hhaI/cfoI
                 nlaIV                  hgiAI/aspHI
                 narI                   bsp1286
                 kasI                   bsiHKAI      mspI
                 hinlI/acyI          cac8I           hpaII
                 hgiCI            fnu4HI            scrFI                  ddeI                     fnu4HI
                 haeII            bsoFI bmyI        nciI                  mnlI   pleI               bsoFI     maeIII      mnlI
                 banI             aciI  apaLI/snoI  dsaV                  eco81I hinfI        ddeI          hphI     bsp1286
            ddeI ahaII/bsaHI nspBII  alw44I/snoI   cauII       scfI      bsu36I/mstII/sauI mnlI bbvI      bstEII   bmyI bpmI/gsuI[dcm-]
1801 TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT
     AGCACCTTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA AGGGCCGACA GGATGTCAGG AGTCCTGAGA TGAGGGAGTC GTCGCACCAC TGGCACGGGA
 162 S  W  N  S   G  A  L   T  S  G   V  H  T  F   P  A  V   L  Q  S   S  G  L  Y   S  L  S   S  V  V   T  V  P  S

         aluI   nlaIV
        fnu4HI  hgiCI                                                       taqI          hgiJII
        bsoFI   banI                 tfiI                                  salI           bsp1286
        bbvI   bsp1286               hinfI                          styI   hincII/hindII  bmyI
     bstXI     bmyI               maeII                             bsaJI  accI           banII        maeIII
1901 CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC
     GGTCGTCGAA CCCGTGGGTC TGGATGTAGA CGTTGCACTT AGTGTTCGGG TCGTTGTGGT TCCAGCTGTT CTTTCAACTC GGGTTTAGAA CACTGTTTTG
 196  S  S  L   G  T  Q   T  Y  I  C   N  V  N   H  K  P   S  N  T  K   V  D  K   K  V  E   P  K  S  C   D  K  T
```

FIG. 41G

```
                                              fnu4HI
                                               bsoFI
                                             haeIII/palI
                                           mcrI
                                           eagI/xmaIII/eclXI
                                           eaeI
                                           cfrI
                                           bsiEI                                 sapI
         cac8I                            notI               rmaI                mboII
       nlaIII                             fnu4HI             maeI                earI/ksp632I                rmaI
      nspI        bsp1286                 bsoFI   nlaIII     bfaI     tth111I/aspI                          maeI
      nspHI  aciI bmyI                    aciI aciI        aluI mnlI        taqI   aluI                     bfaI
2001 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA
     AGTGTGTACG GGCGGCACGG GTCGTGGTCT TGACGACCCG CCGGCGTACT TTGTCGATCT CCTGTTCCAG CTTCTCGATG AGAGGTTCTT GATGGTGGAT
229  H  T  C   P  P  C  P   A  P  E   L  L  G   G  R  M  K   Q  L  E   D  K  V   E  E  L  L   S  K  N   Y  H  L
          ^junction between antibody and leucine zipper

                                                                                                  scrFI
                                              sphI                                                nciI
                                          ddeI nlaIII                                             mspI
                                         celII/espI             rmaI                              hpaII
                                         blpI/bpu1102I          maeI                              dsaV
                                       hinPI   nspI             bfaI  bsmFI                       cauII
                                       hhaI/cfoI             sau96I  pleI                       aciI
                pleI      aluI        haeII    nspHI         haeIII/palI                       fnu4HI
                hinfI    hindIII      eco47III cac8I         asuI    hinfI                     bsoFI
2101 GAGAATGAAG TGGCAAGACT CAAAAAGCTT GTCGGGGAGC GCTAAGCATG CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT
     CTCTTACTTC ACCGTTCTGA GTTTTTCGAA CAGCCCCTCG CGATTCGTAC GCTGCCGGGA TCTCAGGGAT TGCGAGCCAA CGGCGGCCCG CAAAAAATAA
262  E  N  E  V   A  R  L   K  K  L   V  G  E  R   O (SEQ ID NO.60)

     tru9I                        aluI
      mseI                  taqI  hindIII                                                   nlaIV
     hpaI   nlaIII         claI/bsp106 tru9I                     tru9I                       hgiCI
     hincII/hindII   aluI  bspDI[dam-] mseI  aciI                mseI                        banI
2201 GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC
     CAATTGAGTA CAAACTGTCG AATAGTAGCT ATTCGAAATT ACGCCATCAA ATAGTGTCAA TTTAACGATT GCGTCAGTCC GTGGCACATA CTTTAGATTG
```

FIG. 41H

```
                                   sfaNI                                              haeIII/palI
                               scrFI                                            sau96I
                               mvaI                                                 scrFI
                               ecoRII                                         nciI
                               dsaV                                    rsaI   mspI mnlI
                    nlaIV      bstNI                                         csp6I  hpaII
               mnlI hgiCI     bsaJI                                     mspI        dsaV bslI
   hinPI       bsaJI       hphI apyI[dcm+]                              hpaII       cauII             ecoRV
   hhaI/cfoI  fokI    banI maeIII   fokI   scfI                         cfr10I/bsrFI asuI       aciI
2301 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT
     TTACGCGAGT AGCAGTAGGA GCCGTGGCAG TGGGACCTAC GACATCCGTA TCCGAACCAA TACGGCCATG ACGGCCCGGA GAACGCCCTA TAGCAGGTAA

                                  hinPI
                                  hhaI/cfoI
                               rmaI
                               maeI
                              nheI                                                                              fnu4HI
                          fnu4HI haeII                             hinPI           hgiAI/aspHI                  bsoFI
                          bsoFI  eco47III                          hhaI/cfoI       bsp1286        aciI         haeIII/palI
                maeIII    bbvI bfaI                               mstI  bslI       bsiHKAI    mcrI        eaeI
      sfaNI  bsrI      cac8I   cac8I             sfaNI            aviII/fspI       bmyI       bsiEI       cfrI
2401 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG ATGCAATTTC TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG
     GGCTGTCGTA GCGGTCAGTG ATACCGCACG ACGATCGCGA TATACGCAAC TACGTTAAAG ATACGCGTGG GCAAGAGCCT CGTGACAGGC TGGCGAAACC

                                                                                     mnlI
                                                                                   sau3AI
                                                     sau3AI                        mboI/ndeII[dam-]
                                                     mboI/ndeII[dam-]              dpnI[dam+]
                                                     dpnI[dam+]                    dpnII[dam-]
                                                     dpnII[dam-]                   alwI[dam-]
   aciI                                           thaI                            nlaIV
  fnu4HI                                          fnuDII/mvnI                     bstYI/xhoII     hgaI
  bsoFI                                           bstUI  nlaIII                   bamHI        mspI
 aciI   bsrI     cac8I         nlaIV      taqI    bsh1236I          bslI          alwI[dam-]   hpaII  sfaNI
2501 CCGCCGCCCA GTCCTGCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC
     GGCGGCGGGT CAGGACGAGC GAAGCGATGA ACCTCGGTGA TAGCTGATGC GCTAGTACCG CTGGTGTGGG CAGGACACCT AGGAGATGCG GCCTGCGTAG
```

FIG. 41I

```
                 hinPI
                 hhaI/cfoI
                nlaIV
                narI                    hinPI
                kasI                    hhaI/cfoI
                hinlI/acyI              nlaIV                                   hgiJII
     mspI       hgiCI                   narI                                    bsp1286
     hpaII      haeII                   kasI                                    bmyI
    naeI      mspI                      hinlI/acyI                              banII
    cfr10I/bsrFI banI                   hgiCI                             sau3AI cac8I            rcaI  hinPI
    cac8I    sgrAI                      haeII                             mboI/ndeII[dam-]    hgiJII    haeII
   haeIII/palI hpaII                    banI                              dpnI[dam+]          bsp1286   eco47III
  eaeI      hphI ahaII/bsaHI            ahaII/bsaHI                       dpnII[dam-]         bmyI bspHI hhaI/cfoI
  cfrI  sfaNI cfr10I/bsrFI    aciI   cac8I                   hphI       mboII[dam-]          banII nlaIII
2601 GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG
     CACCGGCCGT AGTGGCCGCG GTGTCCACGC CAACGACCGC GGATATAGCG GCTGTAGTGG CTACCCCTTC TAGCCCGAGC GGTGAAGCCC GAGTACTCGC

                                     scrFI
                                     nciI
                                     mspI            hinPI
                                     hpaII           hhaI/cfoI
                                dsaI dsaV            nlaIV
                                bslI cauII           narI
                           sau96I   haeIII/palI      kasI                                  fnu4HI
                           nlaIV  eaeI               hinlI/acyI                            bsoFI hgiAI/aspHI
                           haeIII/palI               hgiCI                                 aciI  bsp1286
                           asuI bsaJI bsaJI          haeII                           fnu4HI   bsiHKAI
                          eco0109I/draII             banI                            bsoFI    bmyI
                        cac8I bslI cfrI    bsmFI     ahaII/bsaHI    cac8I       bslI aciI  aciI        haeIII/palI
2701 CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG GGCGCCATCT CCTTGCACGC ACCATTCCTT GCGGCGGCGG TGCTCAACGG
     GAACAAAGCC GCACCCATAC CACCGTCCGG GGCACCGGCC CCCTGACAAC CCGCGGTAGA GGAACGTGCG TGGTAAGGAA CGCCGCCGCC ACGAGTTGCC

                                                                                                        mspI
                      fnu4HI                                                                            hpaII
                      bsoFI   ecoNI      pleI                                                           bsaWI
    mnlI  bslI   bsrI bbvI    bslI       hinfI             hgaI      sfaNI                  bsrI  aluI bslI
2801 CCTCAACCTA CTACTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG
     GGAGTTGGAT GATGACCCGA CGAAGGATTA CGTCCTCAGC GTATTCCCTC TCGCAGCAGG CTACGGGAAC TCTCGGAAGT TGGGTCAGTC GAGGAAGGCC
```

FIG. 41J

```
                                                                                              fnu4HI
       aciI                                                                                 mspI   hinPI
      thaI                                                                                 naeI   haeII
      fnuDII/mvnI                                                                          cfr10I/bsrFI
      bstUI    nlaIII                                                                      cac8I  eco47III
      bsh1236I               aciI              mboII                                   nlaIV    bsoFI
     hinPI    bcgI          fnu4HI            bpuAI                                    hgiCI    bbvI
     hhaI/cfoI              bsoFI             bbsI         nlaIII                      banI hpaII hhaI/cfoI          mnlI
2901 TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG
     ACCCGCGCCC CGTACTGATA GCAGCGGCGT GAATACTGAC AGAAGAAATA GTACGTTGAG CATCCTGTCC ACGGCCGTCG CGAGACCCAG TAAAAGCCGC

                        thaI
                        fnuDII/mvnI                                                                         sau96I
                        bstUI          haeIII/palI                                                          nlaIV
      aciI              bsh1236I  sau3AI                                                                    avaII
   sau96I              hinPI     mboI/ndeII[dam-]                                                           asuI
   avaII               hhaI/cfoI dpnI[dam+]        aciI        tfiI                                      bsrI    aciI
   asuI         bpmI/gsuI[dcm-]  dpnII[dam-]     cac8I         hinfI    cac8I mnlI                     maeIII  bsmFI
3001 AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC
     TCCTGGCGAA AGCGACCTCG CGCTGCTACT AGCCGGACAG CGAACGCCAT AAGCCTTAGA ACGTGCGGGA GCGAGTTCGG AAGCAGTGAC CAGGGCGGTG

                                                  mcrI
                                                  eagI/xmaIII/eclXI
                                                  eaeI    hinPI
                                                  cfrI    hhaI/cfoI                                 thaI
                                        mspI      bsiEI  thaI                                    hgaI
                                       naeI      fnu4HI  fnuDII/mvnI                          thaI  fnuDII/mvnI
                                       cfr10I/bsrFI      bstUI                                fnuDII/mvnI
                          haeIII/palI hpaII      bsoFI   bsh1236I                             bstUI bstUI
    maeII                 haeI         cac8I     aciI  hgaI                                   bsh1236I mnlI     haeI
   psp1406I            cac8I           bglI nlaIII haeIII/palI      maeII    cac8I     nruI    bsh1236I fokI haeIII/palI
3101 CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC
     GTTTGCAAAG CCGCTCTTCG TCCGGTAATA GCGGCCGTAC CGCCGGCTGC GCGACCCGAT GCAGAACGAC CGCAAGCGCT GCGCTCCGAC CTACCGGAAG
```

FIG. 41K

```
                                                                             bspMI
                                                   thaI                    scrFI
                          fnu4HI                   fnuDII/mvnI             mvaI
                          bsoFI                    bstUI                   ecoRII
           mboII          aciI                cac8I       haeI             dsaV
       tfiI             mspI   mslI    sfaNI   bsh1236I  haeIII/palI       bstNI
       hinfI            hpaII  sfaNI  fokI   aciI    cac8I   nlaIII        apyI[dcm+]                  bsmFI aluI    alwI[dam-]
3201 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG
     GGGTAATACT AAGAAGAGCG AAGGCCGCCG TAGCCCTACG GGCGCAACGT CCGGTACGAC AGGTCCGTCC ATCTACTGCT GGTAGTCCCT GTCGAAGTTC

       fnu4HI
       bsoFI
       aciI
      thaI                           sau96I
      fnuDII/mvnI                    avaII
      bstUI                        bsrI         sau3AI                mnlI
    cac8I                       sau3AI asuI     mboI/ndeII[dam-]      bsaJI    hgiAI/aspHI
sau3AI bsh1236I                 mboI/ndeII[dam-]                    aciI       bsp1286
mboI/ndeII[dam-]                dpnI[dam+] nspBII     maeIII       fnu4HI      bsiHKAI
dpnI[dam+]                      dpnII[dam-]     dpnI[dam+]         bsoFI       bmyI
dpnII[dam-]                   taqI[dam-]     aciI dpnII[dam-]      bglI    cac8I   nlaIII         nlaIII
3301 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTTGGCATG
     CTAGCGAGCG CCGAGAATGG TCGGATTGAA GCTAGTGACC TGGCGACTAG CAGTGCCGCT AAATACGGCG GAGCCGCTCG TGTACCTTGC CCAACCGTAC

         fnu4HI
         bsoFI
       hinPI
       hhaI/cfoI                                             haeIII/palI
      nlaIV                                                 sau96I                          fnu4HI
      narI                                                 scrFI                            bsoFI
      kasI                                   thaI          nciI                             aciI
      hinlI/acyI                   thaI      fnuDII/mvnI   mspI                           mspI     mnlI
      hgiCI                        fnuDII/mvnI             hpaII                          hpaII nlaIV
      haeII                        bstUI     bstUI         dsaV                          naeI   hgiCI
      banI aciI                    bsh1236I  bsh1236I  nlaIV  asuI     taqI              cfr10I/bsrFI
      ahaII/bsaHI              mnlI aciI   hgaI aciI  nlaIII  cauII  mnlI                cac8I  banI
3401 GATTGTAGGC GCCGCCCTAT ACCTTGTCTG CCTCCCCGCG TTGCGTCGCG GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CGGCACCTCG
     CTAACATCCG CGGCGGGATA TGGAACAGAC GGAGGGGCGC AACGCAGCGC CACGTACCTC GGCCCGGTGG AGCTGGACTT ACCTTCGGCC GCCGTGGAGC
```

FIG. 41L

```
                                                                                    hinPI                               hgaI
                                                                                    hhaI/cfoI                          thaI aciI
          hphI                                                                     mstI     pflMI                      fnuDII/mvnI
       tfiI        pflMI                                                            aviII/fspI   styI                  bstUI
       hinfI       bslI      nlaIV                 aciI               bsmI           bslI    bsaJI                     bsh1236I
3501 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC
     GATTGCCTAA GTGGTGAGGT TCTTAACCTC GGTTAGTTAA GAACGCCTCT TGACACTTAC GCGTTTGGTT GGGAACCGTC TTGTATAGGT AGCGCAGGCG

                                                          haeIII/palI
                                                         mscI/balI
                                                         haeI
                                                       scrFI
                                                       mvaI dsaI                                                mspI
                                                       ecoRII                                             hpaII
                                                       dsaV                                              scrFI
                                                       bstNI                                                   nciI
                  fnu4HI                               bslI bsaJI           sau3AI                             dsaV
                 thaI hinPI                            apyI[dcm+]           mboI/ndeII[dam-]                 sau96I
            fnu4HI bsoFI                            sau96I              dpnI[dam+]                       nlaIV
            bsoFI fnuDII/mvnI                       avaII        hinPI  dpnII[dam-]                      avaII          cac8I
        fnu4HI     bstUI                            asuI eaeI    hhaI/cfoI  hgiAI/aspHI                  asuI       rmaI
        bsoFI  cac8I    hhaI/cfoI    fnu4HI        ppuMI       mstI nlaIII bsp1286                      ppuMI       maeI
        bbvI aciI bsh1236I    avaI   bsoFI         nlaIV cfrI      aviII/fspI  bsiHKAI                       eco0109I/draII
    bpmI/gsuI[dcm-] aciI  sfaNI      bbvI          eco0109I/draII  mslI    bmyI              mnlI cauII-bfaI    aciI
3601 CATCTCCAGC AGCCGCACGC GGCGCATCTC GGGCAGCGTT GGGTCCTGGC CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG
     GTAGAGGTCG TCGGCGTGCG CCGCGTAGAG CCCGTCGCAA CCCAGGACCG GTGCCCACGC GTACTAGCAC GAGGACAGCA ACTCCTGGGC CGATCCGACC

                                                                            fnu4HI
                                                  cac8I                     bsoFI
                                                thaI                        bbvI
                                        hphI    fnuDII/mvnI               fnu4HI
                                     tfiI       bstUI                     bsoFI
                bsrI                 hinfI      bsh1236I  maeII           bbvI        maeII      ddeI          nlaIII
3701 CGGGGTTGCC TTACTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA
     GCCCCAACGG AATGACCAAT CGTCTTACTT AGTGGCTATG CGCTCGCTTG CACTTCGCTG ACGACGACGT TTTGCAGACG CTGGACTCGT TGTTGTACTT
```

FIG. 41M

```
                                                                                                 sau3AI
                                                                                                 mboI/ndeII[dam-]
                                                                                                 mamI[dam-]
                                                                                                 dpnI[dam+]
                                                                                                 dpnII[dam-]
                                                                                               bstYI/xhoII
                                                                                               alwI[dam-]
                                                                                             mspI
                                                                                             hpaII
                                                    aciI                                    mroI bsaBI[dam-]       fnu4HI
                                                   thaI                                     bspMII                 bsoFI
                                                   fnuDII/mvnI hinPI                        bspEI[dam-]            bbvI
     mboII                                         bstUI       hhaI/cfoI                    bsaWI      sfaNI     sfaNI
    bpuAI                                                                                   
    bbsI                                           bsh1236I   haeII      mslI               accIII[dam-]        fokI     cac8I
3801 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC
     ACCAGAAGCC AAAGGCACAA AGCATTTCAG ACCTTTGCGC CTTCAGTCGC GGGACGTGGT AATACAAGGC CTAGACGTAG CGTCCTACGA CGACCGATGG

                                                                                      aciI
                                                 cac8I                             bsmFI     fokI
                                               hinPI                               sau96I   sfaNI
                                               hhaI/cfoI                           nlaIV  aciI
                                   tru9I  haeII                                    avaII  fnu4HI           bsrI
                                   mseI   eco47III        ddeI                     asuI   bsoFI        aciI           mnlI
3901 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG TGATTTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA
     GACACCTTGT GGATGTAGAC ATAATTGCTT CGCGACCGTA ACTGGGACTC ACTAAAAAGA GACCAGGGCG GCGTAGGTAT GGCGGTCAAC AAATGGGAGT

                    nspI
                scrFI
                nciI
                mspI
         bsrI   hpaII
         bslI   dsaV nlaIII                                   mnlI
     maeII      cauII                                        fokI
    psp1406I maeIII  nspHI         maeIII            sfaNI                                  nlaIII     apoI    bslI
4001 CAACGTTCCA GTAACCGGGC ATGTTCATCA TCAGTAACCC GTATCGTGAG CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC
     GTTGCAAGGT CATTGGCCCG TACAAGTAGT AGTCATTGGG CATAGCACTC GTAGGAGAGA GCAAAGTAGC CATAGTAATG GGGGTACTTG TCTTTAAGGG
```

FIG. 41N

```
                                                                 cac8I
                                                                 sau96I
                                                        tru9I    haeIII/palI                 tru9I
              sfaNI                                     mseI     asuI                        mseI
           mnlI         maeIII                   aciI bslI  nlaIII aciI                      mseI       bpmI/gsuI[dcm-]
4101 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC
     GGAATGTGCC TCCGTAGTTC ACTGGTTTGT CCTTTTTTGG CGGGAATTGT ACCGGGCGAA ATAGTCTTCG GTCTGTAATT GCGAAGACCT CTTTGAGTTG

                                                                                 fnu4HI   thaI
                                                                                 bsoFI    fnuDII/mvnI
                                                                               aluI       bstUI
                                                                              pvuII      hinPI
                                                                              nspBII     hhaI/cfoI
          aciI                                                               fnu4HI     thaI
         thaI                                                                bsoFI      fnuDII/mvnI
         fnuDII/mvnI                 xmnI                                    bcgI       bstUI
         bstUI                       tfiI                                    bbvI    mnlI bsh1236I
         bsh1236I                    hinfI                                                    
    aluI hgaI  fokI                  asp700         mslI        aluI     aciI bbvI  bsh1236I  hphI      hphI
4201 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG
     CTCGACCTGC GCCTACTTGT CCGTCTGTAG ACACTTAGCG AAGTGCTGGT GCGACTACTC GAAATGGCGT CGACGGAGCG CGCAAAGCCA CTACTGCCAC

                             esp3I
                             bsmBI
                             bsmAI
                          mspI                                  scrFI                    hgaI
                  fnu4HI  hpaII                                 nciI                     thaI
                  bsoFI  scrFI                                  mspI                     fnuDII/mvnI
                  bbvI   nciI                                   hpaII                    bstUI  aciI
               nlaIII    dsaV                                sfaNI                       bsh1236I
              nspI       cauII           aluI               fokI dsaV                    hinPI nspBII
      mnlI    nspHI aluI bslI        maeIII              aciI   cauII    drdI            hhaI/cfoI        aciI
4301 AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA GCGGATGCCG GGAGCAGACA AGCCCGTCAG GGCGCGTCAG CGGGTGTTGG
     TTTTGGAGAC TGTGTACGTC GAGGGCCTCT GCCAGTGTCG AACAGACATT CGCCTACGGC CCTCGTCTGT TCGGGCAGTC CCGCGCAGTC GCCCACAACC
```

FIG. 41O

```
                                                                                                                hgiAI/aspHI
           fnu4HI                                                                                               bsp1286
           bsoFI                  maeII                                                  sfaNI                  bsiHKAI
           bbvI               maeIII                                                  fnu4HI             ddeI   bmyI   ndeI
          hinPI  nlaIII bsrI bsaAI                         bst1107I   tru9I           bsoFI            rsaI     apaLI/snoI
          hhaI/cfoI  tth111I/aspI           aciI           accI bsrI  mseI            aciI             csp6I    alw44I/snoI
4401 CGGGTGTCGG GGCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC
     GCCCACAGCC CCGCGTCGGT ACTGGGTCAG TGCATCGCTA TCGCCTCACA TATGACCGAA TTGATACGCC GTAGTCTCGT CTAACATGAC TCTCACGTGG

                                                                         mboII
                                                                        earI/ksp632I
                                                                       sapI                        hinPI
                                                                     hinPI                         hhaI/cfoI
                                                                     hhaI/cfoI                  fnu4HI
                                                             sfaNI                          pleI  bsoFI     mcrI
         aciI         aciI    sfaNI                        aciI     haeII      aciI  mnlI       hinfI bbvI      bsiEI
4501 ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTCG
     TATACGCCAC ACTTTATGGC GTGTCTACGC ATTCCTCTTT TATGGCGTAG TCCGCGAGAA GGCGAAGGAG CGAGTGACTG AGCGACGCGA GCCAGCAAGC

        fnu4HI
        bsoFI
        aciI                                                                                  nlaIII          bslI
     fnu4HI      aciI                                                                         nspI           cac8I
     bsoFI   bsrBI                                                   tfiI                     nspHI         haeIII/palI
     bbvI  cac8I          aluI           aciI                        hinfI                    aflIII        haeI
4601 GCTGCGGCGA GCGGTATCAG CTCACTCAAA GGCGGTAATA CGGTTATCCA CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAAA AGGCCAGCAA
     CGACGCCGCT CGCCATAGTC GAGTGAGTTT CCGCCATTAT GCCAATAGGT GTCTTAGTCC CCTATTGCGT CCTTTCTTGT ACACTCGTTT TCCGGTCGTT

         scrFI         thaI
         mvaI                fnuDII/mvnI
         ecoRII        bstUI
         dsaV          bsh1236I
         bstNI   bslI      aciI
         apyI[dcm+]       fnu4HI                                                               hgaI
       haeIII/palI        bsoFI   cac8I                      aciI                              drdI
      haeI  nlaIV        haeIII/palI                   nlaIV                     sfaNI         taqI           mnlI
4701 AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT CAGAGGTGGC
     TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA GTCTCCACCG
```

FIG. 41P

```
                                   scrFI
                 scrFI   mvaI
                 mvaI          ecoRII
                 ecoRII  dsaV                                     bslI
                 dsaV    bstNI                   hinPI                  aciI    mspI
                 bstNI         apyI[dcm+]         bssSI                   fnu4HI    hpaII
                 apyI[dcm+]   bsaJI   aluI mnlI   hhaI/cfoI               bsoFI   bsaWI        aciI
4801 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC
     CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA TGGACAGGCG

                                                                                                  hgiAI/aspHI
                                                                                                  bsp1286
                                                                                                  bsiHKAI
              hinPI                                                                               bmyI
              hhaI/cfoI                                                                           apaLI/snoI
             haeII        aluI      scfI       ddeI                                  aluI         alw44I/snoI
4901 CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA
     GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC ACACGTGCTT

                                                                                             alwNI[dcm-]
             fnu4HI                                            mspI                          fnu4HI
             bsoFI                                             hpaII                         bsoFI
           nspBII           maeIII                             scrFI                      fnu4HI
           aciI  hinPI     mspI                                nciI                       bsoFI
        mcrI bbvI          bsaWI                 pleI          dsaV                       bbvI              maeIII
        bsiEI    hhaI/cfoI hpaII                 hinfI         cauII                 bsrI   bbvI   bsrI
5001 CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA
     GGGGGGCAAG TCGGGCTGGC GACGCGGAAT AGGCCATTGA TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCGT CGGTGACCAT

                                                               bslI            rmaI
                                                             haeIII/palI       maeI                   hinPI
               mnlI        aciI   scfI                       haeI              bfaI                   hhaI/cfoI
5101 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC
     TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCC TGTCATAAAC CATAGACGCG
```

FIG. 41Q

```
                                                    mspI
                                                    hpaII
                                                  sau3AI
                                                  mboI/ndeII[dam-]                                    fnu4HI
                                                  dpnI[dam+]                                          bsoFI
                  maeIII                          dpnII[dam-]          nspBII                         bbvI
        eco57I bsrI                         aluI  alwI[dam-]          aciI      aciI                cac8I
5201 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTTGTTTG CAAGCAGCAG
     AGACGACTTC GGTCAATGGA AGCCTTTTTC TCAACCATCG AGAACTAGGC CGTTTGTTTG GTGGCGACCA TCGCCACCAA AAAAACAAAC GTTCGTCGTC

                                        sau3AI
                                  sau3AI  mboI/ndeII[dam-]
                                  mboI/ndeII[dam-]
          hinPI           sau3AI   mboII[dam-] dpnI[dam+]
          hhaI/cfoI       mboI/ndeII[dam-]     dpnII[dam-]
         thaI             dpnI[dam+]   dpnI[dam+]
         fnuDII/mvnI      dpnII[dam-]  dpnII[dam-]                                    tru9I          nlaIII
         bstUI          bstYI/xhoII    alwI[dam-]                                    mseI           rcaI
         bsh1236I       alwI[dam-]  bstYI/xhoII                    hgaI ddeI        maeII          bspHI
5301 ATTACGCGCA GAAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG ATTTTGGTCA
     TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT AGAAAAGATG CCCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC TAAAACCAGT

                               sau3AI
                               mboI/ndeII[dam-]
                             rmaI
                          hphI   dpnI[dam+]
                       mboII[dam-]
                     sau3AI    maeI       tru9I
                     mboI/ndeII[dam-]     mseI
                     dpnI[dam+]   dpnII[dam-]
                     dpnII[dam-]  alwI[dam-]    tru9I          tru9I
                   bstYI/xhoII  bstYI/xhoII    mseI           mseI
                   alwI[dam-] bfaI      ahaIII/draI          ahaIII/draI                                maeIII
5401 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA
     ACTCTAATAG TTTTTCCTAG AAGTGGATCT AGGAAAATTT AATTTTTACT TCAAAATTTA GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT

                       nlaIV            sau3AI
                       hgiCI            mboI/ndeII[dam-]                  pleI
            tru9I      banI             dpnI[dam+]                        hinfI
            mseI     mnlI        ddeI   dpnII[dam-]       fokI            ahdI/eam1105I                    mnlI
5501 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG
     GGTTACGAAT TAGTCACTCC GTGGATAGAG TCGCTAGACA GATAAAGCAA GTAGGTATCA ACGGACTGAG GGGCAGCACA TCTATTGATG CTATGCCCTC
```

FIG. 41R

```
                                        bsmAI
                                        bsaI
                    bsrI                thaI                bpmI/gsuI[dcm-]
                sau96I    fnu4HI        fnuDII/mvnI       mspI                                  mspI
                nlaIV     bsoFI         bstUI             hpaII                                 hpaII   haeIII/palI
                haeIII/palI bsrDI       bsh1236I        cfr10I/bsrFI                          bglI    sau96I hinPI
                asuI      bbvI        aciI          hphI  nlaIV                           cac8I       asuI   hhaI/cfoI
5601 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC
     CCGAATGGTA GACCGGGGTC ACGACGTTAC TATGGCGCTC TGGGTGCGAG TGGCCGAGGT CTAAATAGTC GTTATTTGGT CGGTCGGCCT TCCCGGCTCG

                                                scrFI
                                                nciI
                                                mspI                                          maeII
                                                hpaII    rmaI                                 hinPI
          sau96I                                dsaV     maeI                                 hhaI/cfoI
          avaII                 mnlI    bsrI    mseI     cauII    bfaI                tru9I    mstI psp1406I
          asuI                aciI    fokI      aseI/asnI/vspI    aluI              bsrI mseI     aviII/fspI
5701 GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT
     CGTCTTCACC AGGACGTTGA AATAGGCGGA GGTAGGTCAG ATAATTAACA ACGGCCCTTC GATCTCATTC ATCAAGCGGT CAATTATCAA ACGCGTTGCA

               cac8I                                                                          sau3AI
              scfI                                                                            mboI/ndeII[dam-]
              pstI                                                                            dpnI[dam+]
             fnu4HI                                                    nlaIV      sau3AI     dpnII[dam-]
             bsoFI                                                     mspI       mboI/ndeII[dam-]
             bbvI    mslI                                              bsaWI      dpnI[dam+]      nlaIII     nlaIII
        bsrDI bsgI  sfaNI      maeIII                                  aluI hpaII dpnII[dam-] maeIII  alwI[dam-]
5801 TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC
     ACAACGGTAA CGACGTCCGT AGCACCACAG TGCGAGCAGC AAACCATACC GAAGTAAGTC GAGGCCAAGG GTTGCTAGTT CCGCTCAATG TACTAGGGGG

                                    sau3AI
                                    mboI/ndeII[dam-]          aciI
                                    dpnI[dam+]                fnu4HI
                                 mnlI dpnII[dam-]             bsoFI
                               sau96I pvuI/bspCI              haeIII/palI                    fnu4HI
                               avaII  mcrI                    eaeI              nlaIII       bsoFI
                    aciI   aluI      asuI   bsiEI             cfrI              mslI         bbvI
5901 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA
     TACAACACGT TTTTTCGCCA ATCGAGGAAG CCAGGAGGCT AGCAACAGTC TTCATTCAAC CGGCGTCACA ATAGTGAGTA CCAATACCGT CGTGACGTAT
```

FIG. 41S

```
                                                                                         mcrI
                                                                                         bsiEI
                                                                                         bcgI
                                                      rsaI                            fnu4HI
                 fokI                          bsrI   scaI                            bsoFI
            nlaIII          sfaNI       maeIII hphI csp6I                ddeI         aciI
6001 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC
     TAAGAGAATG ACAGTACGGT AGGCATTCTA CGAAAAGACA CTGACCACTC ATGAGTTGGT TCAGTAAGAC TCTTATCACA TACGCCGCTG GCTCAACGAG

          hgaI
         hinlI/acyI
         ahaII/bsaHI             hinPI                                                                      sau3AI
       mspI                      hhaI/cfoI                                                                  mboI/ndeII[dam-]
        hpaII                   thaI                           hgiAI/aspHI                                  dpnI[dam+]
      scrFI                     fnuDII/mvnI                    bsp1286           maeII                      dpnII[dam-]
      nciI                      bstUI                    tru9I bsiHKAI          psp1406I                    bstYI/xhoII
      dsaV                      bsh1236I                 mseI  bmyI           xmnI                          alwI[dam-]
      cauII hincII/hindII      aciI                    ahaIII/draI            asp700   mboII
6101 TTGCCCGGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC
     AACGGGCCGC AGTTGTGCCC TATTATGGCG CGGTGTATCG TCTTGAAATT TTCACGAGTA GTAACCTTTT GCAAGAAGCC CCGCTTTTGA GAGTTCCTAG

                 bsrI                        hgiAI/aspHI
               sau3AI   taqI                 bsp1286          eco57I
               mboI/ndeII[dam-]              bsiHKAI        mboII[dam-]
               dpnI[dam+]                    bmyI         sau3AI   sfaNI
               dpnII[dam-]                   apaLI/snoI   mboI/ndeII[dam-]
      nspBII   alwI[dam-]                    alw44I/snoI  dpnI[dam+]
      aciI    bstYI/xhoII     maeIII    bssSI             dpnII[dam-]            hphI           hphI
6201 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG
     AATGGCGACA ACTCTAGGTC AAGCTACATT GGGTGAGCAC GTGGGTTGAC TAGAAGTCGT AGAAAATGAA AGTGGTCGCA AAGACCCACT CGTTTTTGTC

              aciI
             fnu4HI                                                  mboII
             bsoFI                    mslI                         earI/ksp632I   sspI
6301 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA
     CTTCCGTTTT ACGGCGTTTT TTCCCTTATT CCCGCTGTGC CTTTACAACT TATGAGTATG AGAAGGAAAA AGTTATAATA ACTTCGTAAA TAGTCCCAAT
```

FIG. 41T

```
                                                                                                  hinPI
                                                                                                 thaI
                                                                                                 fnuDII/mvnI
                                                                                                 bstUI                                  maeII
          nlaIII                                                                                 bsh1236I                               hinlI/acyI
         rcaI                                                                                   aciI                                   ahaII/bsaHI
         bspHI  aciI                                                                          nlaIV  hhaI/cfoI                         aatII ddeI
       bsmAI  bsrBI
6401 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC GCGCACATTT CCCCGAAAAG TGCCACCTGA CGTCTAAGAA
     AACAGAGTAC TCGCCTATGT ATAAACTTAC ATAAATCTTT TTATTTGTTT ATCCCCAAGG CGCGTGTAAA GGGGCTTTTC ACGGTGGACT GCAGATTCTT

                                                                 sau96I
                                                                 haeIII/palI
                                                                 asuI       mboII
                 nlaIII                                         eco0109I/draII
                rcaI    tru9I                                  mnlI        bpuAI
                bspHI   mseI                                  bssSI        bbsI
6501 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC CTTTCGTCTT CAA  (SEQ ID NO:61)
     TGGTAATAAT AGTACTGTAA TTGGATATTT TTATCCGCAT AGTGCTCCGG GAAAGCAGAA GTT
```

FIG. 41U

```
>length: 6563

aatII(GACGTC):              1645 6489
acc65I(GGTACC):             403 823
accI(GTMKAC):               1093 1963 4449
accIII(TCCGGA):             3867[dam-]
aciI(CCGC):                 178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
                            2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
                            3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
                            4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
                            5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
acyI                        see hinlI
aflIII(ACRYGT):             1307 4678
ageI(ACCGGT):               1788
ahaII/bsaHI(GRCGYC):        1645 1813 2616 2637 2751 3408 6107 6489
ahaIII/draI(TTTAAA):        5435 5454 6146
ahdI/eam1105I(GACNNNNNGTC): 346 5566
aluI(AGCT):                 72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
                            2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
                            5922
alw44I/snoI(GTGCAC):        1831 4494 4992 6238
alwI[dam-](GGATC):          412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
                            6196 6214
alwNI[dcm-](CAGNNNCTG):     1117 1385 5089
apaI(GGGCCC):               1695
apaLI/snoI(GTGCAC):         1831 4494 4992 6238
apoI(RAATTY):               1 391 4093
apyI[dcm+](CCWGG):          640 999 1347 1357 1449 1665 1713 1755 1764 2333 3262 3645 4705 4826 4839
aseI/asnI/vspI(ATTAAT):     5742
asnI                        see aseI
asp700(GAANNNNTTC):         905 930 4234 6166
asp718(GGTACC):             403 823
aspHI                       see hgiAI
aspI                        see tth111I
asuI(GGNCC):                1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463
```

FIG. 41V

Stop Template Primer

SL.97.2 5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3' (SEQ ID NO.63)

NNS Randomization Primer

SL.97.3 5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3' (SEQ ID NO.64)

FIG. 42

Randomization of Position N35 of Variable Light Chain CDR-1
Amino Acid Frequency

Phage Display (NNS Codon Library) Sort #3

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

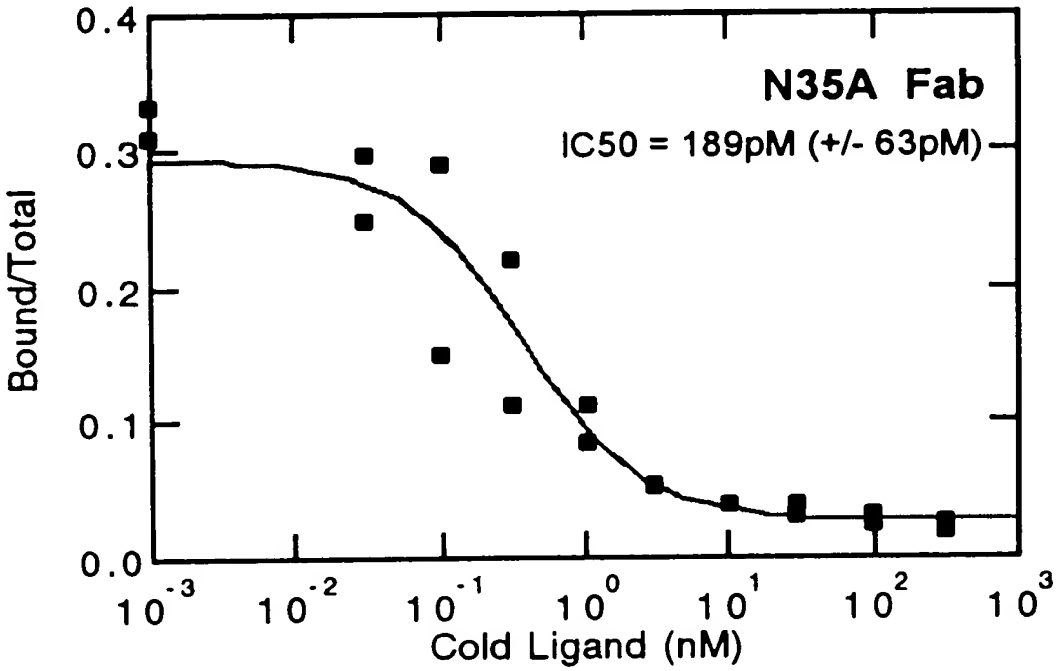


FIG. 43B

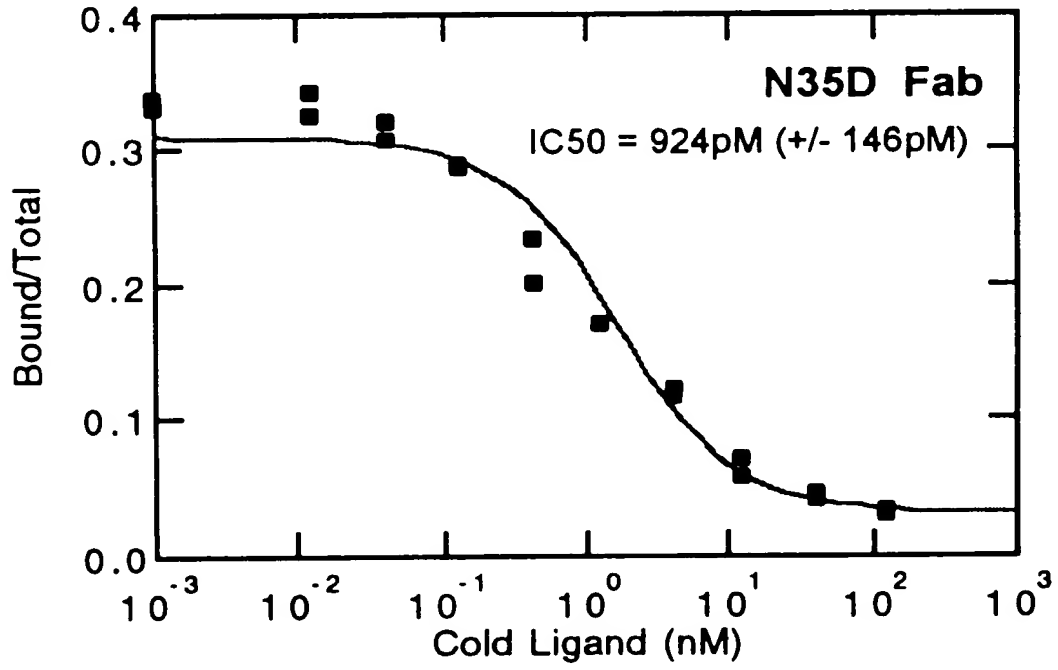


FIG. 43C

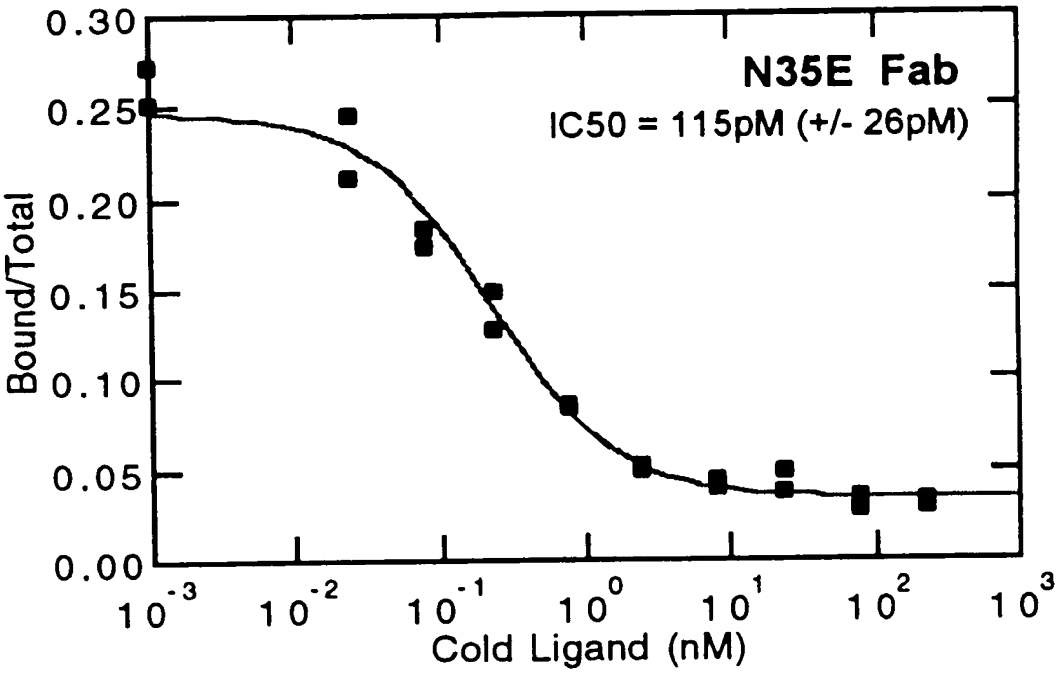


FIG. 43D

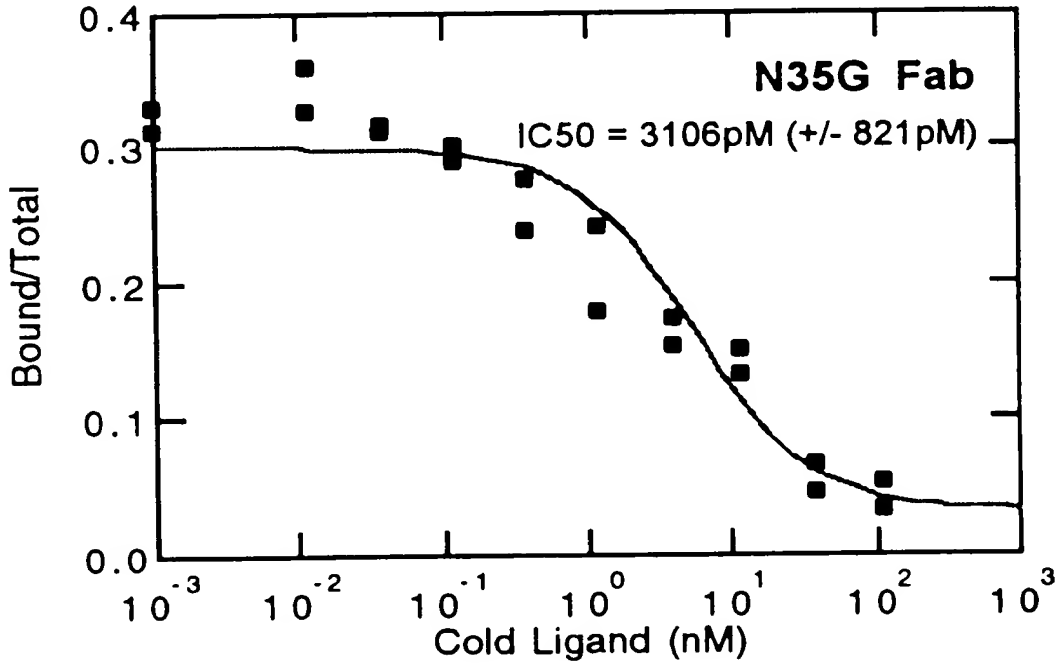
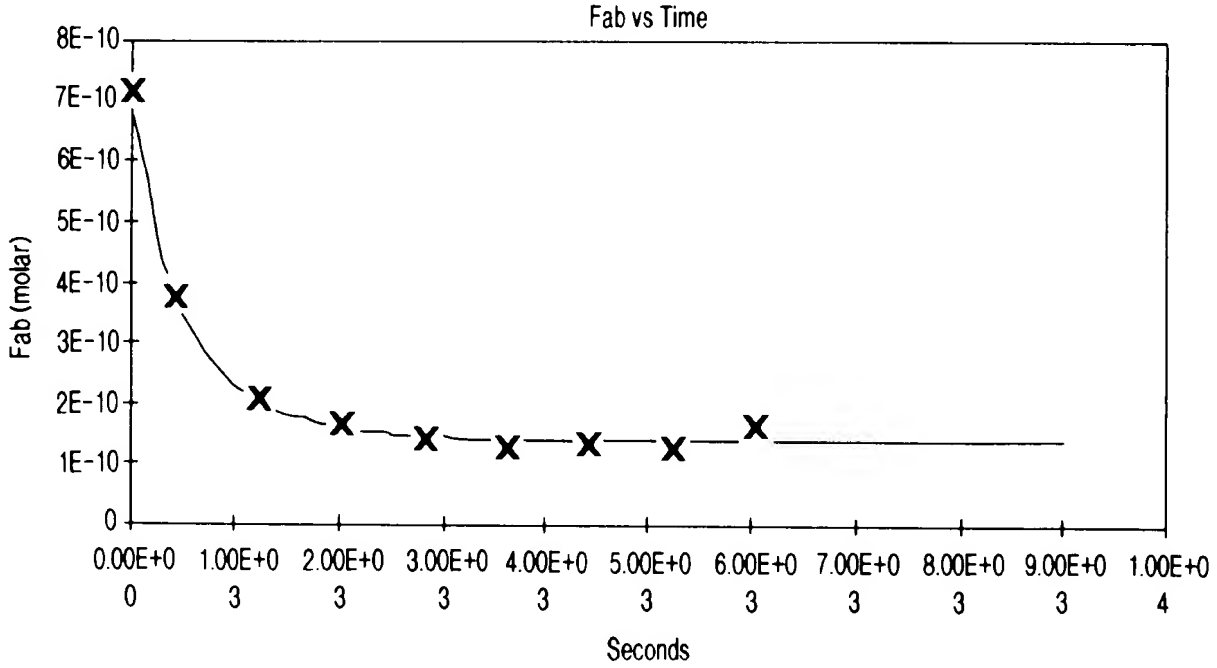


FIG. 43E



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')2.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab')$_2$	2.0×10^6	2.1×10^{-4}	109pM
6G4V11N35E-Fab	4.7×10^6	2.6×10^{-4}	54pM

FIG. 44

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M  K  K  N    I  A  F    L  L  A    S  M  F  V    F  S  I    A  T  N

 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
    CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
 -3 A  Y  A  D    I  Q  M    T  Q  S    P  S  S  L    S  A  S    V  G  D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT
    TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA
 18 R  V  T  I    T  C  R  S  S  Q    S  L  V  H    G  I  G    E  T  Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
    AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
 38 L  H  W  Y    Q  Q  K    P  G  K    A  P  K  L    L  I  Y    K  V  S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
    TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
 58 N  R  F  S    G  V  P    S  R  F    S  G  S  G    S  G  T    D  F  T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT
    GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
 78 L  T  I  S    S  L  Q    P  E  D    F  A  T  Y    Y  C  S  Q  S  T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
    GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
 98 H  V  P  L  T    F  G    Q  G  T    K  V  E  I    K  R  T    V  A  A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
    GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P  S  V  F    I  F  P    P  S  D    E  Q  L  K    S  G  T    A  S  V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
    CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V  C  L  L    N  N  F    Y  P  R    E  A  K  V    Q  W  K    V  D  N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
    CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A  L  Q  S    G  N  S    Q  E  S    V  T  E  Q    D  S  K    D  S  T

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
    ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y  S  L  S    S  T  L    T  L  S    K  A  D  Y    E  K  H    K  V  Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
    CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT
198 A  C  E  V    T  H  Q    G  L  S    S  P  V  T    K  S  F    N  R  G
                                                                (SEQ ID NO.65)
721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
    CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E  C  O (SEQ ID NO.62)
```

FIG. 45

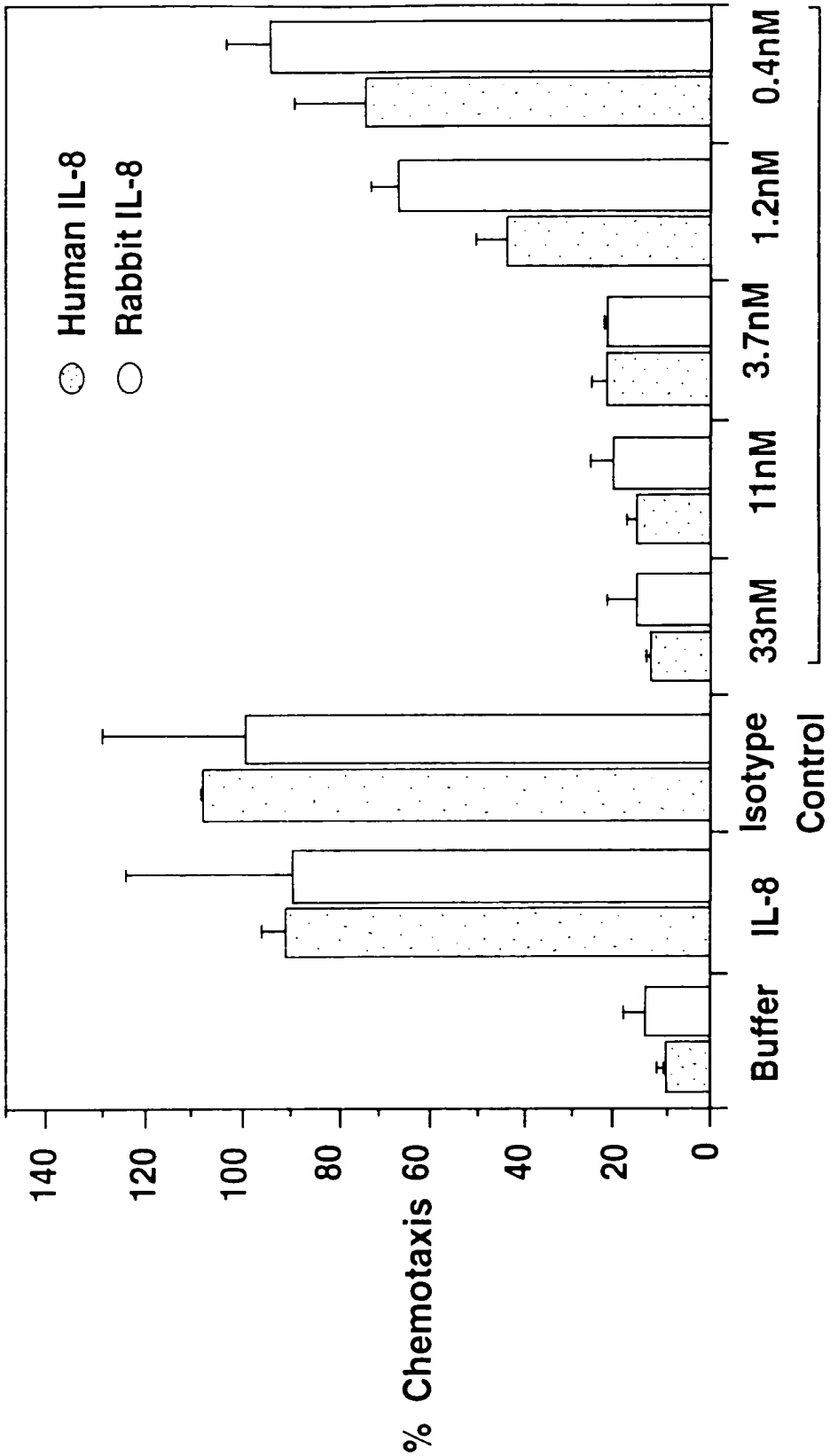


FIG. 46

N35AH1upr

5'-CTAGTGCAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTCCTTC-3'
(SEQ ID NO.66)

N35AH1lwr

5'-TCGAGAAGGAGTAGCCAGAAGCTGCACAGGACAAACGGAGTGAGCCCCCTGGCTGCACCAGGCCACCGCCAGACTGCACT
AG-3'
(SEQ ID NO.67)

Bold indicates nucleotide change destroying PvuII site.

FIG. 47

```
> length: 8120 (circular)
>This has the pSVI backbone with the pRK7 cloning linker (pSVI7) and the intron DHFR(ID)
>made from pSVI.WTSD.D by adding a linearization linker(LL) into the Hpal site

         cac8I
        aluI
       sstI
       sacI                                sau3AI  aluI
       hgiJII                              mboI/ndeII[dam-]                                   scrFI
       hgiAI/aspHI                         dpnI[dam+]                                         mvaI
       ecl136II                           pvuI/bspCI                                          ecoRII
       bsp1286                        pleI dpnII[dam-]                                        dsaV
       bsiHKAI                        hinfI  taqI[dam-]                                       bstNI
       bmyI                       rmaI    mcrI    pvuII                                       apyI[dcm+]
       banII                      maeI    bsiEI   nspBII                                     bsaJI
     taqI                         bfaI   taqI[dam-]                                      bsmFI   nlaIV     cac8I
  1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA
    AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCTCAGCTAG CTGTCGACAC CTTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG GGTCGTCCGT

                     sfaNI                                    scrFI                            sfaNI
                   ppu10I                  scrFI        mvaI                                 ppu10I
                   nsiI/avaIII             mvaI               ecoRII                         nsiI/avaIII
                  nlaIII                   ecoRII       dsaV                          nlaIII
                 sphI                      dsaV         bstNI                              sphI
                 nspI                      bstNI              apyI[dcm+]                         nspI
                 nspHI                     apyI[dcm+]       bsaJI                              nspHI
                 cac8I                    sexAI         bsmFI   nlaIV     cac8I                cac8I
101 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
    CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTTC AGGGGTCCGA GGGGTCGTCC GTCTTCATAC GTTTCGTACG TAGAGTTAAT

                                                                                        nlaIII
                                                                                       styI
                                                                                       ncoI
                     aciI                   aciI                                  bslI dsaI
                  bsmFI           aciI  fokI             aciI bsrI  aciI          aciI bsaJI
201 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT
    CAGTCGTTGG TATCAGGGCG GGGATTGAGG CGGGTAGGGC GGGGATTGAG GCGGGTCAAG GCGGGTAAGA GGCGGGGTAC CGACTGATTA AAAAAAATAA
```

FIG. 48A

```
                                                                               rmaI
                                                                               maeI
                    fnu4HI                                                    styI                             haeIII/palI
                    bsoFI                                                     bsaJI                  aluI     mcrI
                    bglI                                                      blnI                 rmaI       eagI/xmaIII/eclXI
                   sfiI                                                       avrII[dam-]          maeI       eaeI
                   haeIII/palI                                              haeIII/palI            bfaI       cfrI
                 mnlI   mnlI      ddeI                       mnlI          stuI                   nheI        bsiEI
            haeIII/palI bsaJI  mnlI   aluI               mnlI              haeI                   cac8I      mspI
          mnlI bsaJI aciI    haeIII/palI                 bseRI            mnlI bfaI              aluI        hpaII
301 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG
    ATACGTCTCC GGCTCCGGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAAA AAACCTCCGG ATCCGAAAAC GTTTTTCGAT CGAATAGGCC

                              tfiI
    scrFI                     hinfI
    nciI                   aciI                                                                      fnu4HI
    mspI                  thaI                                                                       bsoFI
    hpaII                 fnuDII/mvnI                         aciI                                   bbvI
    dsaV                  bstUI                   maeII  rsaI                                      nspBII
    cauII                 bsh1236I             maeIII    csp6I  scfI            mnlI             aciI        nlaIII
401 CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT
    GGCCCTTGCC ACGTAACCTT GCGCCTAAGG GGCACGGTTC TCACTGCATT CATGGCGGAT ATCTCGCTAT TCTCCTAAAA TAGGGGCGAC GGTAGTACCA
                                                   ^splice donor                                    DHFR ATG^

                                                                              haeIII/palI
                                                                             haeI
                                                                           scrFI
                                                                           mvaI     bsrBI
                                                                           ecoRII
                                                                           dsaV
                                     pflMI                                 bstNI    aciI                     rsaI
                                     bslI                        bsmAI     apyI[dcm+]        xmnI            csp6I
    taqI           sfaNI         bsmFI                           bsaI     bsaJI  mnlI  ddeI  asp700         scaI
501 TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAAATATG GGGATTGGCA AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC
    AGCTGGTAAC TTGACGTAGC AGCGGCACAG GGTTTTATAC CCCTAACCGT TCTTGCCTCT GGATGGGACC GGAGGCGAGT CCTTGCTCAA GTTCATGAAG
```

FIG. 48B

```
                                                                                 scrFI
                                                                                 mvaI
                                                                                 ecoRII
           eco57I                                                                dsaV
          mboII                     tfiI                                         bstNI                  tfiI       tru9I
         earI/ksp632I               hinfI   hphI                                 apyI[dcm+]             hinfI      mseI
        mnlI                      alwNI[dcm-]                                   sexAI              ddeI mboII taqI  ahaIII/draI
601 CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA
    GTTTCTTACT GGTGTTGGAG AAGTCACCTT CCATTTGTCT TAGACCACTA ATACCCATCC TTTTGGACCA AGAGGTAAGG ACTCTTCTTA GCTGGAAATT

                                                                   sstI
                                                                   sacI
                                                                   hgiJII
                                                                   hgiAI/aspHI
                                                                   ecl136II
                                                                   bsp1286
                                                                   bsiHKAI
                                                                   bmyI
                                                               mnlI aluI                                   tru9I
       tru9I                                                bssSI  banII                                  aflII/bfrI
       mseI          ddeI                                                                                 
      aseI/asnI/vspI                                     bslI   bseRI           bstXI      fokI sfaNI mseI
701 AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA
    TCCTGTCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGGTGGTGCT CCTCGAGTAA AAGAACGGTT TTCAAACCTA CTACGGAATT CTGAATAACT

                                                                                                haeIII/palI
                                                                                               haeI
                                                                            scrFI        scrFI
                                                                            mvaI               mvaI
                                                                            ecoRII       ecoRII
     mspI                                                                   dsaV   tfiI  dsaV
     hpaII                                                                  bstNI   nlaIII     bstNI    ddeI pleI
    bsaWI                 accI nlaIII           mnlI                        apyI[dcm+] hinfI   apyI[dcm+]    hinfI
801 ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT
    TGTTGGCCTT AACCGTTCAT TTCATCTGTA CCAAACCTAT CAGCCTCCGT CAAGACAAAT GGTCCTTCGG TACTTAGTTG GTCCGGTGGA ATCTGAGAAA
```

FIG. 48C

FIG. 48D

```
                                                                              dsaV                          ecoRI
                                                                              bstNI                          taqI   apoI
        maeIII                                                                apyI[dcm+]      mnlI          claI/bsp106
        hphI   scfI      fokI                                          bslI   bsaJI           bsaJI         bspDI[dam-]
1201 ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT
     TATGCTAAAT CCACTGTGAT ATCTATTGTA GGTGAAACGG AAAGAGAGGT GTCCACAGGT GAGGGTCCAG GTTGACGTGG AGCCAAGATA GCTAACTTAA
                                                                   seq from pRK6G425VH: Cla-AvrII^

                                                                                                    scrFI
                                                                                                    mvaI  fnu4HI
                                                                                                    ecoRII
                                                                                                    dsaV
                                                                                     rmaI           bstNI bsoFI
                                                                     rsaI            maeI           apyI[dcm+]
                                              rmaI         bpmI/gsuI[dcm-]           bfaI        haeI      bbvI
      nlaIII                                  maeI                                                 aciI haeIII/palI
      styI                                                                      aluI
      pflMI
      ncoI
      dsaI
      bslI fokI
      bsaJI     nlaIII   fokI                 bfaI         bsrI   csp6I
1301 CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA
     GGTGGTACCC TACCAGTACA TAGTAGGAAA AAGATCATCG TTGACGTTGA CCTCATGTAA GTCTTCAAGT CGATCACGTC AGACCGCCAC CGGACCACGT
   1                                                                  E  V  Q   L  V  Q   S  G  G  G   L  V  Q

                                                                                           scrFI
                                                                                           nciI
                                                                                           mspI
                                                                                           hpaII
                                                                                           dsaV
                                                                                           cauII
                                                                                          xmaI/pspAI
                                                                                          smaI
                                                                                          scrFI
                                                                                          nciI
                                                                                          dsaV         scrFI
                                                                                          cauII        mvaI
                                                                                          bslI         ecoRII
       hgiJII                                                                             bsaJI        dsaV
       bsp1286                                                                       avaI        bstNI
       bmyI                                                                              bsaJI        bslI
     scrFI                                                     pleI
     mvaI banII                                           hinfI              sau96I    sau96I          apyI[dcm+]
     ecoRII                     aluI                                         avaII     nlaIV          haeIII/palI
     dsaV                       alwNI[dcm-]              taqI                      asuI     haeIII/palI  sau96I
     bstNI                         fnu4HI                    xhoI                 nlaIV     asuI bslI    eco0109I/draII
     bsaJI                         bsoFI                     paeR7I            bsrI      eco0109I/draII asuI
     apyI[dcm+]                    bbvI                      avaI  maeIII
1401 GCCAGGGGGC TCACTCCGTT TGTCCTGTGC AGCTTCTGGC TACTCCTTCT CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCGGGTAA GGGCCTGGAA
     CGGTCCCCCG AGTGAGGCAA ACAGGACACG TCGAAGACCG ATGAGGAAGA GCTCAGTGAT ATACGTGACC CAGGCAGTCC GGGGCCCATT CCCGGACCTT
  14  P  G  G   S  L  R  L   S  C  A   A  S  G   Y  S  F  S   S  H  Y   M  H  W   V  R  Q  A   P  G  K   G  L  E
```

FIG. 48E

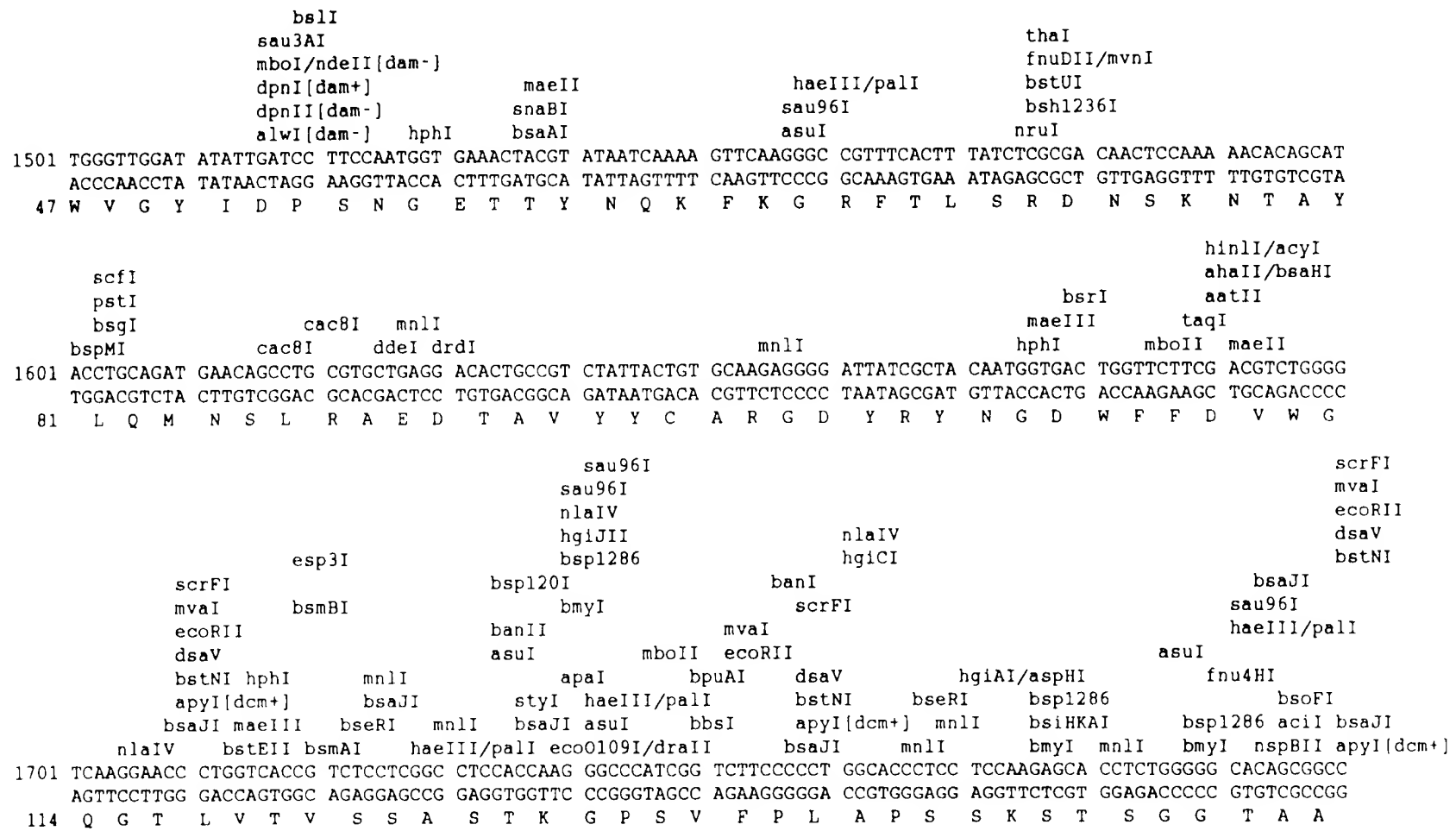


FIG. 48F

```
            scrFI
            mvaI
            ecoRII
            ecoNI                                               hinPI
            dsaV                                          nlaIV              hgiAI/aspHI
            bstNI                                               narI              bsp1286
            bslI                           maeIII          kasI              bsiHKAI
            apyI[dcm+]                        hphI              hinlI/acyI        bmyI        mspI
          fnu4HI                            mspI                hgiCI           cac8I        hpaII
          bsoFI                             hpaII               haeII        fnu4HI          scrFI
          bbvI                             cfr10I/bsrFI        banI         bsoFI           nciI
                                  bslI     bsaWI               ahaII/bsaHI  aciI apaLI/snoI dsaV
                                           ageI  tth111I/aspI  ddeI hhaI/cfoI nspBII alw44I/snoI cauII  scfI
1801 CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC
     GACCCGACGG ACCAGTTCCT GATGAAGGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGGACTGGT CGCCGCACGT GTGGAAGGGC CGACAGGATG
 147 L  G  C  L   V  K  D   Y  F  P   E  P  V  T   V  S  W   N  S  G   A  L  T  S   G  V  H   T  F  P   A  V  L  Q

                                                        fnu4HI
                                                        bsoFI     nlaIV
          ddeI pleI              fnu4HI               rmaI       hgiCI
         mnlI  hinfI             bsoFI       bsp1286 maeI        banI                     tfiI
         eco81I            mnlI  bbvI     maeIII     bfaI   aluI bsp1286                  hinfI
         bsu36I/mstII/sauI  ddeI        hphI   bmyI mnlI  bbvI   bmyI              maeII
1901 AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACTGT GCCCTCTAGC AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA
     TCAGGAGTCC TGAGATGAGG GAGTCGTCGC ACCACTGACA CGGGAGATCG TCGAACCCGT GGGTCTGGAT GTAGACGTTG CACTTAGTGT TCGGGTCGTT
 181  S  S  G   L  Y  S   L  S  S  V   V  T  V   P  S  S   S  L  G  T   Q  T  Y   I  C  N   V  N  H  K   P  S  N

                                                                                         ahdI/eam1105I
                                                                                        sau96I
                                                                                        avaII
                                                                                  scrFI
                                                                                  mvaI    asuI
                                                                                  ecoRII
                             hgiJII                                               dsaV
        styI                 bsp1286                     nlaIII                   bstNI  nlaIV       mboII
        bsaJI                bmyI                      nspI       bsp1286         bsaJI  bsmFI       bpuAI
      mslI                   banII        maeIII       nspHI      bmyI alwNI[dcm-] apyI[dcm+]        bbsI mnlI
2001 CACCAAGGTG GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC
     GTGGTTCCAC CTGTTCTTTC AACTCGGGTT TAGAACACTG TTTTGAGTGT GTACGGGTGG CACGGGTCGT GGACTTGAGG ACCCCCCTGG CAGTCAGAAG
 214  T  K  V   D  K  K  V   E  P  K   S  C  D   K  T  H  T   C  P  P   C  P  A   P  E  L  L   G  G  P   S  V  F
```

FIG. 48G

```
                                              sau96I
                                              nlaIV
                                            mspI
                                            hpaII
                                           scrFI
                                           nciI
                                           dsaV
                                       sau3AI   avaII                  nlaIII
                                       mboI/ndeII[dam-]                nspI
                                   nlaIII    cauII       mnlI          nspHI                       drdI    mnlI
                                  rcaI dpnI[dam+]      ddeI          mslI                     mboII   ddeI
                              mnlI    dpnII[dam-]     eco81I maeIII                         bpuAI  eco81I
     mboII          styI     mslI bspHI[dam-]    asuI bsu36I/mstII/sauI          maeII        bbsI   bsu36I/mstII/sauI
     earI/ksp632I   bsaJI
2101 CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA GGTCACATGC GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT
     GAGAAGGGGG GTTTTGGGTT CCTGTGGGAG TACTAGAGGG CCTGGGGACT CCAGTGTACG CACCACCACC TGCACTCGGT GCTTCTGGGA CTCCAGTTCA
247  L  F  P  P   K  P  K   D  T  L   M  I  S  R   T  P  E   V  T  C   V  V  V  D   V  S  H   E  D  P   E  V  K  F

                                                    aciI
                                                   thaI
                                                   fnuDII/mvnI
                                                   bstUI
                                                   bsh1236I
                                                  sacII/sstII
                                                  nspBII
                                                  kspI
                                                  dsaI
                                                  bsaJI                            rsaI
                                                  aciI                             csp6I
          maeII                                  fnu4HI    mnlI     rsaI          maeII                      hphI
        rsaI                                      bsoFI    bseRI    csp6I         bsaAI          hgaI  mnlI
        csp6I
     bsrI bsaAI            mnlI
2201 TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAAGCCG CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT
     AGTTGACCAT GCACCTGCCG CACCTCCACG TATTACGGTT CTGTTTCGGC GCCCTCCTCG TCATGTTGTC GTGCATGGCA CACCAGTCGC AGGAGTGGCA
281   N  W  Y   V  D  G   V  E  V  H   N  A  K   T  K  P   R  E  E  Q   Y  N  S   T  Y  R   V  V  S  V   L  T  V

          scrFI
          mvaI
          ecoRII
          dsaV                                                                                          fnu4HI
     ecoNI bstNI bsrI                   rsaI       bsmAI                                                     bsoFI
     bslI  apyI[dcm+]                   csp6I      bsaI            mnlI            taqI                      bbvI
2301 CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA ACAAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCAA AGCCAAAGGG
     GGACGTGGTC CTGACCGACT TACCGTTCCT CATGTTCACG TTCCAGAGGT TGTTTCGGGA GGGTCGGGGG TAGCTCTTTT GGTAGAGGTT TCGGTTTCCC
314   L  H  Q   D  W  L  N   G  K  E   Y  K  C   K  V  S  N   K  A  L   P  A  P   I  E  K  T   I  S  K   A  K  G
```

FIG. 48H

```
                                      scrFI
                                      nciI
                                      mspI
                                      hpaII
                                      dsaV
                                      cauII
                                     xmaI/pspAI
                                     smaI
                                     scrFI                    scrFI          scrFI
                                     nciI                     mvaI                 mvaI
                                     dsaV                     ecoRII         ecoRII
                        rsaI         cauII                    dsaV           dsaV
                        csp6I      fokI                       bstNI                bstNI
                                bslI  bsaJI  mboII            apyI[dcm+]           apyI[dcm+]
        avaI          bsp1407I/bsrGI bslI avaI  earI/ksp632I  sexAI           bspMI
2401 CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCCATCCC GGGAAGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA
     GTCGGGGCTC TTGGTGTCCA CATGTGGGAC GGGGGTAGGG CCCTTCTCTA CTGGTTCTTG GTCCAGTCGG ACTGGACGGA CCAGTTTCCG AAGATAGGGT
347  Q  P  R  E   P  Q  V   Y  T  L   P  P  S  R   E  E  M   T  K  N   Q  V  S  L   T  C  L   V  K  G   F  Y  P  S

                                  mspI
                                  hpaII
             dsaI               fnu4HI
             bslI               bsoFI                                    pleI                   mnlI
      mslI bsaJI        bsrDI   bbvI                   mnlI              hinfI    nlaIV  mboII   scfI cac8I
2501 GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG
     CGCTGTAGCG GCACCTCACC CTCTCGTTAC CCGTCGGCCT CTTGTTGATG TTCTGGTGCG GAGGGCACGA CCTGAGGCTG CCGAGGAAGA AGGAGATGTC
381   D  I  A   V  E  W   E  S  N  G   Q  P  E   N  N  Y   K  T  T  P   P  V  L   D  S  D   G  S  F  F   L  Y  S

                                      mboII
                                     bpuAI                   nlaIII
            dsaI               fnu4HI  maeII               ppu10I                              sapI
         hphI                  bsoFI  xmnI bbsI            nsiI/avaIII                         mboII mnlI
       aluI  bsaJI      bspMI  bbvI   asp700      nlaIII   sfaNI   mnlI                        earI/ksp632I
2601 CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC
     GTTCGAGTGG CACCTGTTCT CGTCCACCGT CGTCCCCTTG CAGAAGAGTA CGAGGCACTA CGTACTCCGA GACGTGTTGG TGATGTGCGT CTTCTCGGAG
414   K  L  T   V  D  K  S   R  W  Q   Q  G  N   V  F  S  C   S  V  M   H  E  A   L  H  N  H   Y  T  Q   K  S  L
```

FIG. 48I

```
                                                                                  sau96I
                                                                         aciI     haeIII/palI
        scrFI                           taqI                             fnu4HI   asuI
        nciI                         pleI                                bsoFI nlaIII
        mspI                      rmaI salI    scfI                     sfiI   styI
        hpaII                     maeI hincII/hindII                   eaeI   ncoI                    aluI
        dsaV                   sau96I  hinfI   pstI                    cfrI   dsaI                   fnu4HI
    bsmAI                      haeIII/palI     bsgI               aluI haeIII/palI                   bsoFI
 bslI   cauII                  asuI bfaI accI bspMI             hindIII bglI bsaJI                   bbvI        maeIII
2701 TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA
     AGGGACAGAG GCCCATTTAC TCACGCTGCC GGGATCTCAG CTGGACGTCT TCGAACCGGC GGTACCGGGT TGAACAAATA ACGTCGAATA TTACCAATGT
447  S  L  S  P   G  K  O  (SEQ ID NO.71)

                                                                    rmaI
                                                                    maeI
            sfaNI   apoI                                       bsmI bfaI                                         nlaIII alwI[dam-]
2801 AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG
     TTATTTCGTT ATCGTAGTGT TTAAAGTGTT TATTTCGTAA AAAAAGTGAC GTAAGATCAA CACCAAACAG GTTTGAGTAG TTACATAGAA TAGTACAGAC

    sau3AI
    mboI/ndeII[dam-]
    dpnI[dam+]
    dpnII[dam-]
   pvuI/bspCI
   mcrI
   bsiEI                                                                               rsaI
  taqI[dam-]  tru9I                                                                    csp6I
 claI/bsp106[dam-]       fnu4HI    haeI                                               nlaIV
 bspDI[dam-]  mseI       bsoFI styI                                                   kpnI
sau3AI     xmnI          bbvI  ncoI                                                   hgiCI
mboI/ndeII[dam-]       hinPI   dsaI haeIII/palI                                       banI
dpnI[dam+] asp700      hhaI/cfoI nlaIII                                               asp718     mnlI
dpnII[dam-]  aseI/asnI/vspI    bsaJI              mnlI      mnlI                      acc65I  ddeI  aciI
2901 GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG
     CTAGCTAGCC CTTAATTAAG CCGCGTCGTG GTACCGGACT TTATTGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTTCT TGGTAGACAC
```

FIG. 48J

```
                                    scrFI                        sfaNI
                                    mvaI                            ppu10I                 scrFI
                                    ecoRII                     nsiI/avaIII           mvaI
                                    dsaV                      nlaIII                 ecoRII
                                    bstNI                          sphI                    dsaV
                                    apyI[dcm+]                     nspI                    bstNI
                                   bsaJI                           nspHI                   apyI[dcm+]
                               bsmFI   nlaIV    cac8I              cac8I                  sexAI         bsmFI
3001 GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG
     CTTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG GGTCGTCCGT CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTTC

          nlaIV                           sfaNI
        scrFI                      ppu10I
        mvaI                            nsiI/avaIII
        ecoRII                    nlaIII
        dsaV                     sphI
        bstNI                          nspI
        apyI[dcm+]                     nspHI                      aciI                  aciI
       bsaJI        cac8I              cac8I                  bsmFI         aciI  fokI          aciI
3101 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC
     AGGGGTCCGA GGGGTCGTCC GTCTTCATAC GTTTCGTACG TAGAGTTAAT CAGTCGTTGG TATCAGGGCG GGGATTGAGG CGGGTAGGGC GGGGATTGAG

                                                                      fnu4HI
                                                                      bsoFI
                                                                      bglI
                               nlaIII                                sfiI
                              styI                                   haeIII/palI
                              ncoI                                 mnlI   mnlI    ddeI
                         bslI dsaI                             haeIII/palI bsaJI mnlI  aluI           mnlI
        bsrI  aciI       aciI bsaJI                        mnlI bsaJI aciI  haeIII/palI               bseRI
3201 CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG
     GCGGGTCAAG GCGGGTAAGA GGCGGGGTAC CGACTGATTA AAAAAAATAA ATACGTCTCC GGCTCCGGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC
```

FIG. 48K

```
                                                   scrFI
                                                   nciI
                                                   mspI
                   rmaI                            hpaII
                   maeI                            dsaV
                  styI                          haeIII/palI
                  bsaJI                aluI     mcrI                         tfiI
                  blnI               rmaI       eagI/xmaIII/eclXI            hinfI
                  avrII[dam-]        maeI       eaeI                      aciI
                haeIII/palI          bfaI       cfrI                     thaI
               stuI                 nheI        bsiEI                    fnuDII/mvnI
               haeI                 cac8I      mspI cauII                bstUI               pleI
      mnlI     mnlI bfaI           aluI        hpaII                     bsh1236I            hinfI
3301 AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA
     TCCTCCGAAA AAACCTCCGG ATCCGAAAAC GTTTTTCGAT CGAATAGGCC GGCCCTTGCC ACGTAACCTT GCGCCTAAGG GGCACGGTTC TCAGTCCATT
                  ^seq from pSVI6B5-6G4VL: AvrII - HindIII frag                U1 matched splice donar^

                                                                                         sau3AI
                                                                                         mboI/ndeII[dam-]
                                                                                         dpnI[dam+]
                                                                                         dpnII[dam-]
                                                                                         alwI[dam-]
                                                                                      taqI[dam-]
                                                                                     claI/bsp106[dam-]
                                                fnu4HI                               bspDI[dam-]
                                                bsoFI                               sau3AI
                                 bstXI          aciI                                mboI/ndeII[dam-]
       aciI            scfI  sau96I    styI    thaI                                 dpnI[dam+]
    rsaI        pleI         haeIII/palI       fnuDII/mvnI tru9I                    dpnII[dam-]
    csp6I  scfI hinfI        asuI      bsaJI   bsh1236I      mseI                  alwI[dam-]                fokI
3401 GTACCGCCTA TAGAGTCTAT AGGCCCACCC CCTTGGCTTC GTTAGAACGC GGCTACAATT AATACATAAC CTTTTGGATC GATCCTACTG ACACTGACAT
     CATGGCGGAT ATCTCAGATA TCCGGGTGGG GGAACCGAAG CAATCTTGCG CCGATGTTAA TTATGTATTG GAAAACCTAG CTAGGATGAC TGTGACTGTA
                                     ^sp6 promoter                         ^removed ATG
                                                                                      ^U2 match
                                                                                 lariat consensus^
                                                                         IgG vH natural lariat restored^
```

FIG. 48L

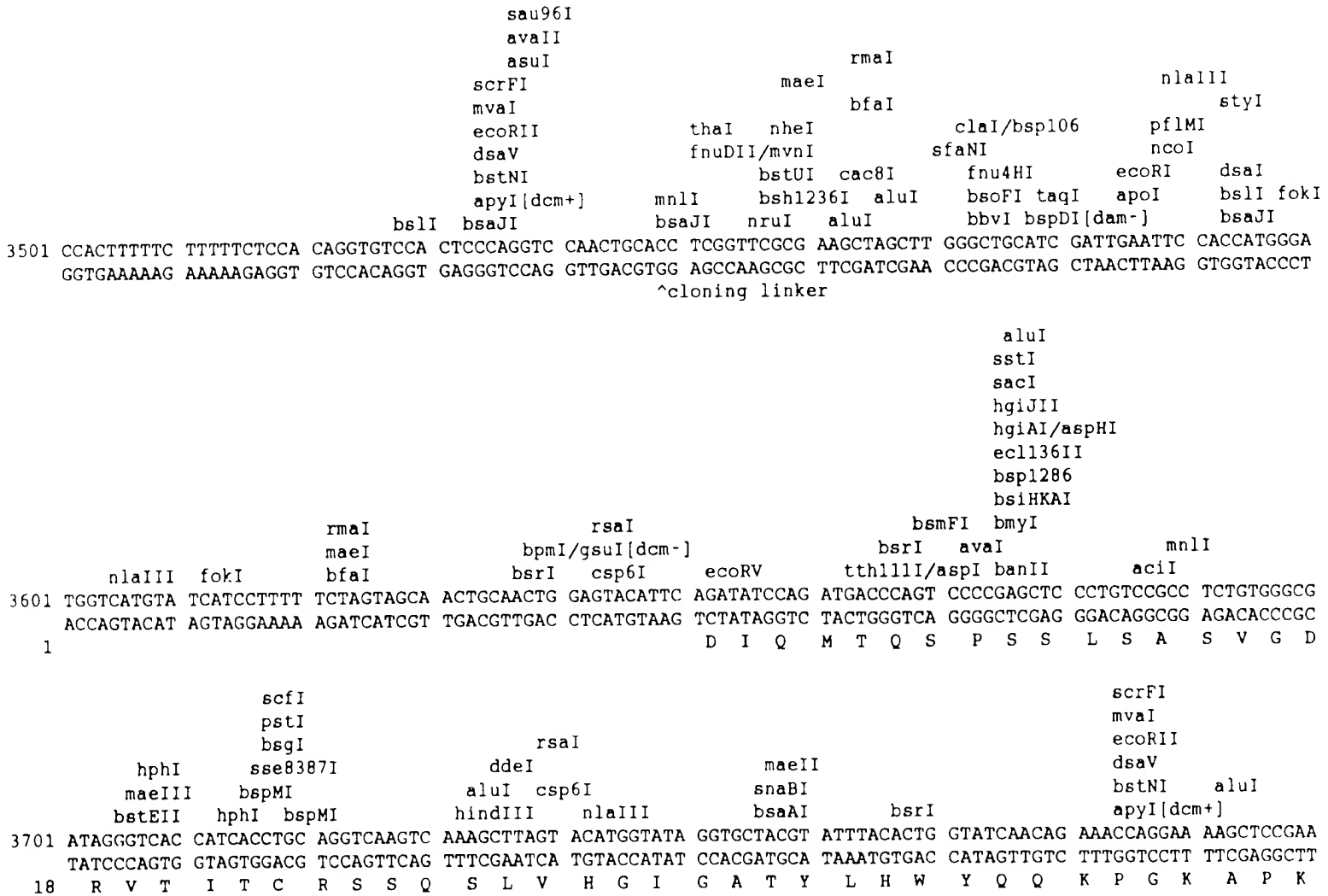


FIG. 48M

```
                                                                     mspI
                                                                     hpaII
                                                                     bslI
                                                                    bsaWI
                                                                  sau3AI
                                                                  mboI/ndeII[dam-]
                                                                  dpnI[dam+]
                                                                  dpnII[dam-]
                                                                  alwI[dam-]                          fnu4HI
                                   tfiI                          nlaIV                                 bsoFI
                                  hinfI        bsmFI             bstYI/xhoII                           bbvI
                                 taqI      bpmI/gsuI[dcm-]       bamHI                                scfI
                                claI/bsp106 pleI                 alwI[dam-]    bsmFI                  pstI
                                bspDI[dam-] hinfI                                                     bsgI
3801 ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT TCTCTGGATC CGGTTCTGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG
     TGATGACTAA ATGTTTCATA GGTTAGCTAA GAGACCTCAG GGAAGAGCGA AGAGACCTAG GCCAAGACCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC
  51  L  L  I   Y  K  V  S   N  R  F   S  G  V   P  S  R  F   S  G  S   G  S  G   T  D  F  T   L  T  I   S  S  L

                                                                              rsaI
                                                                              csp6I
                                                                             nlaIV
                                                                             kpnI styI
                                                       bsrBI                 hgiCI           sau3AI
      mboII                             rsaI           aciI                  banI bsaJI      mboI/ndeII[dam-] fnu4HI
      bpuAI                             csp6I        bsmFI                   asp718          dpnI[dam+]        bsoFI
      bbsI                             scaI     nlaIII          maeII        acc65I          dpnII[dam-]       bbvI
3901 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG
     GTCGGTCTTC TGAAGCGTTG AATAATGACA AGTGTCTCAT GAGTACAGGG CGAGTGCAAA CCTGTCCCAT GGTTCCACCT CTAGTTTGCT TGACACCGAC
  84 Q  P  E  D   F  A  T   Y  Y  C   S  Q  S  T   H  V  P   L  T  F   G  Q  G  T   K  V  E   I  K  R   T  V  A  A

                                                                                                       haeIII/palI
        mboII                                                                                          haeI
       bpuAI                                             xmnI                        xmnI              mnlI
       bbsI    mboII  aciI                               asp700             cac8I    asp700
4001 CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
     GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGAAGAC AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT
 118   P  S  V   F  I  F   P  P  S  D   E  Q  L   K  S  G   T  A  S  V   V  C  L   L  N  N   F  Y  P  R   E  A  K
```

FIG. 48N

```
                                           scrFI
                                           mvaI
                                           ecoRII
                                           dsaV
                                           bstNI                                                    fnu4HI
      rsaI                mnlI             apyI[dcm+]                                   ddeI  bsoFI
      csp6I               bslI    maeIII  bsaJI      maeIII                     scfI   mnlI  bbvI
4101  AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
      TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG AGGGTCCTCT CACAGTGTCT CGTCCTGTCG TTCCTGTCGT GGATGTCGGA GTCGTCGTGG
151   V  Q  W   K  V  D  N   A  L  Q   S  G  N   S  Q  E  S   V  T  E   Q  D  S   K  D  S  T   Y  S  L   S  S  T

                                                                          sstI
                                                                          sacI
                                                                          hgiJII
                                                                          hgiAI/aspHI
                                                                          ecl136II
                                                                          bsp1286
                                                                          bsiHKAI
                                                                          bmyI
                                                                        ddeI cac8I
                                                                      haeIII/palI
                                                                     sau96I aluI
       ddeI                                                          asuI  banII
      celII/espI                                             hphI   eco0109I/draII
      blpI/bpu1102I                                  accI   cac8I  maeIII  alwNI[dcm-]      maeIII   aluI
   hgaI
4201  CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
      GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC
184  L  T  L  S   K  A  D   Y  E  K   H  K  V  Y   A  C  E   V  T  H   Q  G  L  S   S  P  V   T  K  S   F  N  R  G

                        sau96I
                  aciI  haeIII/palI
                 fnu4HI asuI
                 bsoFI nlaIII
                 sfiI  styI
             aluI haeIII/palI                   aluI
            hindIII bglI ncoI                  fnu4HI
           tru9I  eaeI  dsaI                   bsoFI
           mseI   cfrI  bsaJI                  bbvI       maeIII              sfaNI  apoI
4301  GAGAGTGTTA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT
      CTCTCACAAT TCGAACCGGC GGTACCGGGT TGAACAAATA ACGTCGAATA TTACCAATGT TTATTTCGTT ATCGTAGTGT TTAAAGTGTT TATTTCGTAA
218    E  C  O (SEQ ID NO.72)
```

FIG. 48O

```
                                                                              sau3AI
                                                                              mboI/ndeII[dam-]
                                                                              dpnI[dam+]
                                                                              dpnII[dam-]
                                                                             pvuI/bspCI
                                                                             mcrI
                                                                             bsiEI
                                                                            taqI[dam-]
                                                                           claI/bsp106[dam-]
                                                                           bspDI[dam-]  tru9I      fnu4HI    haeI
                                                                          sau3AI        mseI       bsoFI styI
                                                                          mboI/ndeII[dam-]         bbvI  ncoI
                  rmaI                                                    dpnI[dam+] xmnI         hinPI  dsaI haeIII/palI
                  maeI                                                    dpnII[dam-]  aseI/asnI/vspI    bsaJI
            bsmI  bfaI                                            nlaIII alwI[dam-]  asp700        hhaI/cfoI nlaIII
4401 TTTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA
     AAAAAGTGAC GTAAGATCAA CACCAAACAG GTTTGAGTAG TTACATAGAA TAGTACAGAC CTAGCTAGCC CTTAATTAAG CCGCGTCGTG GTACCGGACT
                                                                                 ^sv40

                              rsaI                                                                      scrFI
                               csp6I                                                                    mvaI
                              nlaIV                                                                     ecoRII
                              kpnI                                                                      dsaV
                              hgiCI                                                                     bstNI
                              banI                        aluI                                          apyI[dcm+]
                              asp718     mnlI            pvuII                                         bsaJI
        mnlI      mnlI        acc65I   ddeI   aciI       nspBII                                    bsmFI   nlaIV
4501 AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC
     TTATTGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTTCT TGGTCGACAC CTTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG

                            sfaNI                                             scrFI                      sfaNI
                          ppu10I                scrFI          mvaI                                    ppu10I
                          nsiI/avaIII           mvaI                          ecoRII                   nsiI/avaIII
                         nlaIII                 ecoRII         dsaV                               nlaIII
                        sphI                    dsaV           bstNI                                   sphI
                        nspI                    bstNI                  apyI[dcm+]                           nspI
                        nspHI                   apyI[dcm+]            bsaJI                                 nspHI
      cac8I             cac8I                  sexAI            bsmFI    nlaIV      cac8I                   cac8I
4601 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC
     GGTCGTCCGT CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTTC AGGGGTCCGA GGGGTCGTCC GTCTTCATAC GTTTCGTACG
```

FIG. 48P

```
                                                                                                    nlaIII
                                                                                                   styI
                                                                                                   ncoI
                                 aciI                    aciI                                 bslI dsaI
                              bsmFI           aciI   fokI             aciI bsrI  aciI         aciI bsaJI
4701 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT
     TAGAGTTAAT CAGTCGTTGG TATCAGGGCG GGGATTGAGG CGGGTAGGGC GGGGATTGAG GCGGGTCAAG GCGGGTAAGA GGCGGGGTAC CGACTGATTA

                                                                                            rmaI
                                                                                            maeI
                                fnu4HI                                                     styI
                                bsoFI                                                      bsaJI
                                bglI                                                       blnI
                               sfiI                                                        avrII[dam-]
                               haeIII/palI                                               haeIII/palI
                             mnlI   mnlI      ddeI                       mnlI           stuI
                        haeIII/palI bsaJI  mnlI   aluI               mnlI               haeI                      maeIII
                      mnlI bsaJI aciI    haeIII/palI                 bseRI             mnlI bfaI              aluI
4801 TTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTG
     AAAAAAATAA ATACGTCTCC GGCTCCGGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAAA AAACCTCCGG ATCCGAAAAC GTTTTTCGAC
                                                                                                 start pUC118^

                  fnu4HI
                 haeIII/palI       hinPI
                mcrI               hhaI/cfoI
                eagI/xmaIII/eclXI thaI
                eaeI              fnuDII/mvnI
              notI                bstUI                                                                          scrFI
            bsrBI bsoFI          hinPI               bspMI                                                       mvaI
          taqI  cfrI             hhaI/cfoI         scfI                                                          ecoRII
         xhoI fnu4HI   tru9I     cac8I     tru9I   pstI                     haeIII/palI                          dsaV
         paeR7I bsiEI  pacI     ascI      ahaIII/draI                     eaeI                                   bstNI
         avaI bsoFI    mseI tru9I bsh1236I mseI    bsgI  maeIII           cfrI                      bsrI         apyI[dcm+]
        mnlI  aciI aciI     mseI bssHII  swaI     sse8387I     aluI      bsrI               maeII maeIII        bsaJI
4901 TTACCTCGAG CGGCCGCTTA ATTAAGGCGC GCCATTTAAA TCCTGCAGGT AACAGCTTGG CACTGGCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC
     AATGGAGCTC GCCGGCGAAT TAATTCCGCG CGGTAAATTT AGGACGTCCA TTGTCGAACC GTGACCGGCA GCAAAATGTT GCAGCACTGA CCCTTTTGGG
       ^linearization linker inserted into Hpal site
```

FIG. 48Q

```
                                                                                                               sau3AI
                                                                                                               mboI/ndeII[dam-]
                                                                                                    sau96I     dpnI[dam+]
                                                                     cac8I                          haeIII/palI
                                                                    aluI                            asuI       dpnII[dam-]
                                        fnu4HI                      pvuII                         mnlI aciI   pvuI/bspCI
                    tru9I               bsoFI                       nspBII                     mboII cac8I    mcrI
         maeIII     mseI                bbvI      fokI             cac8I                       earI/ksp632I   bsiEI
5001 TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCCC TTCGCCAGCT GGCGTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT
     ACCGCAATGG GTTGAATTAG CGGAACGTCG TGTAGGGGGG AAGCGGTCGA CCGCATTATC GCTTCTCCGG GCGTGGCTAG CGGGAAGGGT TGTCAACGCA

                      hinPI
                      hhaI/cfoI
                     nlaIV
                     narI
                     kasI                                                                                          hinPI
                     hinlI/acyI                                                                                   thaI
                     hgiCI                                                                                        fnuDII/mvnI
                     haeII      aciI                                                                              bstUI scfI
                     banI     sfaNI                                                                               bsh1236I
      bglI           ahaII/bsaHI                        sfaNI    aciI          aciI   maeII              rsaI hhaI/cfoI
                                                                                                         csp6I    bslI
5101 AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACGCGCCCTG
     TCGGACTTAC CGCTTACCGC GGACTACGCC ATAAAAGAGG AATGCGTAGA CACGCCATAA AGTGTGGCGT ATGCAGTTTC GTTGGTATCA TGCGCGGGAC

                        aciI
                     fnu4HI                      fnu4HI
                     bsoFI                       bsoFI
                    thaI                       hinPI                                     hinPI
                    fnuDII/mvnI                hhaI/cfoI                                 hhaI/cfoI
           hinPI    bstUI                     thaI                                   rmaI
           hhaI/cfoI hinPI                    fnuDII/mvnI                        hinPI  haeII
        fnu4HI       hhaI/cfoI                bstUI                              hhaI/cfoI    bsrBI
        bsoFI      tru9I aciI                 bsh1236I      aciI                haeII maeI    aciI
        aciI       mseI bsh1236I          maeIII bbvI   maeIII          cac8I       bfaI  cac8I             mboII
5201 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC
     ATCGCCGCGT AATTCGCGCC GCCCACACCA CCAATGCGCG TCGCACTGGC GATGTGAACG GTCGCGGGAT CGCGGGCGAG GAAAGCGAAA GAAGGGAAGG
```

FIG. 48R

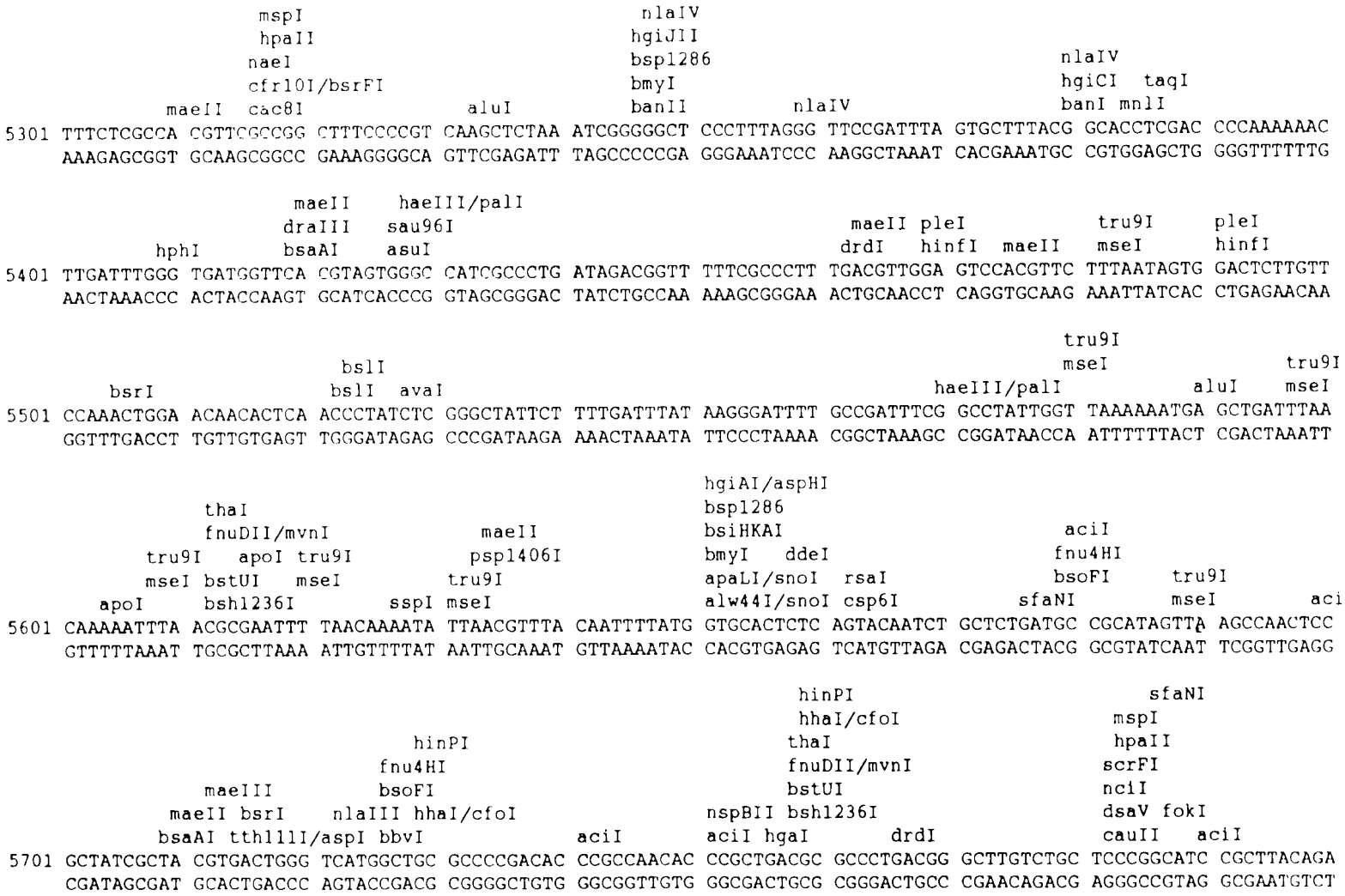


FIG. 48S

```
                                                                    thaI
                                                                    fnuDII/mvnI
                 scrFI                                              bstUI
                 nciI                                               bsh1236I
                 mspI                                              hinPI
                 hpaII     nspI                                    hhaI/cfoI                   mnlI
                 dsaV      nspHI                                  thaI mnlI                   haeIII/palI
             esp3I       fnu4HI                                   fnuDII/mvnI       mboII    sau96I
             bsmBI       bsoFI                                    bstUI             bpuAI    asuI bssSI
        maeIII bsmAI     bbvI                                     bsh1236I          bbsI    eco0109I/draII
     aluI      bslI  cauII aluI nlaIII    mnlI     hphI      hphI
5801 CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCACCGTC ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA
     GTTCGACACT GGCAGAGGCC CTCGACGTAC ACAGTCTCCA AAAGTGGCAG TAGTGGCTTT GCGCGCTCCG TCATAAGAAC TTCTGCTTTC CCGGAGCACT

                                                                                      nlaIV
                                                                                   aciI
                                                                                  thaI
                                                                                  fnuDII/mvnI
                                                          hinlI/acyI              bstUI
                           nlaIII                         ahaII/bsaHI             bsh1236I
                     tru9I  rcaI                          aatII                  hinPI
                     mseI   bspHI                    ddeI maeII                  hhaI/cfoI
5901 TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT
     ATGCGGATAA AAATATCCAA TTACAGTACT ATTATTACCA AAGAATCTGC AGTCCACCGT GAAAAGCCCC TTTACACGCG CCTTGGGGAT AAACAAATAA

                               rcaI
                               bspHI
                           bsrBI    bsmAI                                      mboII
                           aciI  nlaIII                             sspI       earI/ksp632I           mslI
6001 TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC
     AAAGATTTAT GTAAGTTTAT ACATAGGCGA GTACTCTGTT ATTGGGACTA TTTACGAAGT TATTATAACT TTTTCCTTCT CATACTCATA AGTTGTAAAG

                                                                                                      hgiAI/aspHI
                                                                                                      bsp1286
                                                                                            sau3AI    bsiHKAI
                                                                                            mboI/ndeII[dam-]
                                                                                            dpnI[dam+] bmyI
                          fnu4HI                                                            dpnII[dam-]
                          bsoFI                                                        eco57I         apaLI/snoI
                          aciI                              hphI           hphI         sfaNI  mboII[dam-]   alw44I/snoI
6101 CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG
     GCACAGCGGG AATAAGGGAA AAAACGCCGT AAAACGGAAG GACAAAAACG AGTGGGTCTT TGCGACCACT TTCATTTTCT ACGACTTCTA GTCAACCCAC
```

FIG. 48T

```
                          sau3AI    nspBII     sau3AI
                          mboI/ndeII[dam-]     mboI/ndeII[dam-]               maeII
                          dpnI[dam+]           dpnI[dam+]                    psp1406I            hgiAI/aspHI
                         bstYI/xhoII           dpnII[dam-]                  xmnI                 bsp1286  tru9I
                     bsrI dpnII[dam-]          alwI[dam-]                   asp700               bsiHKAI  mseI
      bssSI    maeIII taqI   alwI[dam-]  aciI  bstYI/xhoII               mboII                   bmyI   ahaIII/draI
6201 CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT
     GTGCTCACCC AATGTAGCTT GACCTAGAGT TGTCGCCATT CTAGGAACTC TCAAAAGCGG GGCTTCTTGC AAAAGGTTAC TACTCGTGAA AATTTCAAGA

                                    scrFI
           aciI                     nciI
          thaI                      mspI
          fnuDII/mvnI               hpaII
          bstUI                     dsaV
          bsh1236I               hinlI/acyI                  aciI                                 rsaI
         hinPI                   hgaI cauII            mcrI  fnu4HI                               csp6I   bsrI
         hhaI/cfoI               ahaII/bsaHI     bcgI  bsiEI bsoFI        ddeI                    scaI  hphI  maeIII
6301 GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC
     CGATACACCG CGCCATAATA GGGCACTACT GCGGCCCGTT CTCGTTGAGC CAGCGGCGTA TGTGATAAGA GTCTTACTGA ACCAACTCAT GAGTGGTCAG

                                                                                                       sau3AI
                                                                                   haeIII/palI         mboI/ndeII[dam-]
                                                                                  eaeI                 dpnI[dam+]
                                                                                  cfrI                 dpnII[dam-]
                                                       fnu4HI                     fnu4HI              pvuI/bspCI
                                                       bsoFI                      bsoFI               mcrI
         sfaNI     fokI    nlaIII                      bbvI  mslI  nlaIII         aciI                bsiEI
6401 ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA
     TGTCTTTTCG TAGAATGCCT ACCGTACTGT CATTCTCTTA ATACGTCACG ACGGTATTGG TACTCACTAT TGTGACGCCG GTTGAATGAA GACTGTTGCT

                                                     nlaIII
                                                  sau3AI maeIII                       mspI
      sau96I                                      mboI/ndeII[dam-]       sau3AI   nlaIV
      avaII                                       dpnI[dam+]             mboI/ndeII[dam-] aluI
      asuI                                        dpnII[dam-]            dpnI[dam+]   hpaII
    mnlI          aluI    aciI              nlaIII alwI[dam-]            dpnII[dam-] bsaWI
6501 TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA
     AGCCTCCTGG CTTCCTCGAT TGGCGAAAAA ACGTGTTGTA CCCCCTAGTA CATTGAGCGG AACTAGCAAC CCTTGGCCTC GACTTACTTC GGTATGGTTT
```

FIG. 48U

```
                                   hinPI                                          mspI
                                   hhaI/cfoI                                      hpaII
                 fnu4HI           mstI                                       aluI  scrFI
                 bsoFI            aviII/fspI      bsrI                       rmaI  nciI        tru9I
          mslI    cac8I  bsrDI   maeII          tru9I                        maeI  dsaV        mseI
      maeIII    sfaNI   bbvI    psp1406I        mseI                         bfaI  cauII       aseI/asnI/vspI
6601 CGACGAGCGT GACACCACGA TGCCAGCAGC AATGGCAACA ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA
     GCTGCTCGCA CTGTGGTGCT ACGGTCGTCG TTACCGTTGT TGCAACGCGT TTGATAATTG ACCGCTTGAT GAATGAGATC GAAGGGCCGT TGTTAATTAT

                                   bglI                                            mspI
                                   sau96I     cac8I                                hpaII
                  sau96I           haeIII/palI                                    cfr10I/bsrFI
   fokI    aciI   avaII      hinPI asuI   mspI                               nlaIV hphI         bsmAI
 bsrI   mnlI      asuI       hhaI/cfoI    hpaII                          bpmI/gsuI[dcm-]        bsaI
6701 GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT
     CTGACCTACC TCCGCCTATT TCAACGTCCT GGTGAAGACG CGAGCCGGGA AGGCCGACCG ACCAAATAAC GACTATTTAG ACCTCGGCCA CTCGCACCCA

  aciI
 thaI        fnu4HI     haeIII/palI
 fnuDII/mvnI bsoFI     sau96I                                         pleI
 bstUI       bbvI     nlaIV                                           hinfI
 bsh1236I bsrDI   bsrI asuI          mnlI                        ahdI/eam1105I         fokI
6801 CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG
     GAGCGCCATA GTAACGTCGT GACCCCGGTC TACCATTCGG GAGGGCATAG CATCAATAGA TGTGCTGCCC CTCAGTCCGT TGATACCTAC TTGCTTTATC

     ddeI
  sau3AI       nlaIV
  mboI/ndeII[dam-]                                                                  tru9I
  dpnI[dam+]   hgiCI        tru9I                                                   mseI           tru9I
  dpnII[dam-]  banI mnlI    mseI       maeIII                                       ahaIII/draI    mseI
6901 ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA
     TGTCTAGCGA CTCTATCCAC GGAGTGACTA ATTCGTAACC ATTGACAGTC TGGTTCAAAT GAGTATATAT GAAATCTAAC TAAATTTTGA AGTAAAAATT

        rmaI
        maeI      sau3AI
      sau3AI hphI mboI/ndeII[dam-]
      mboI/ndeII[dam-]
      dpnI[dam+]  dpnI[dam+]
      dpnII[dam-] dpnII[dam-]                                                                          sau3AI
 tru9I bstYI/xhoII  alwI[dam-]     nlaIII         maeII                                                mboI/ndeII[dam-]
 mseI  alwI[dam-]  bstYI/xhoII     rcaI          tru9I                  hgaI                           dpnI[dam+]
ahaIII/draI bfaI  mboII[dam-]      bspHI         mseI                ddeI                              dpnII[dam-]
7001 TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA
     AAATTTTCCT AGATCCACTT CTAGGAAAAA CTATTAGAGT ACTGGTTTTA GGGAATTGCA CTCAAAAGCA AGGTGACTCG CAGTCTGGGG CATCTTTTCT
```

FIG. 48V

```
                             sau3AI
                   mboII[dam-]
                 sau3AI      mboI/ndeII[dam-] thaI                                                                         sau3AI
                 mboI/ndeII[dam-]             fnuDII/mvnI                                                                  mboI/ndeII[dam-]
                 dpnI[dam+]  dpnI[dam+]       bstUI        cac8I                                                           dpnI[dam+]
                 dpnII[dam-] dpnII[dam-]      bsh1236I  fnu4HI                                                             dpnII[dam-]
                bstYI/xhoII  alwI[dam-]      hinPI      bsoFI                                 aciI            mspI        alwI[dam-]
                alwI[dam-]  bstYI/xhoII      hhaI/cfoI  bbvI                       aciI     nspBII          hpaII      aluI
7101 TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA
     AGTTTCCTAG AAGAACTCTA GGAAAAAAAG ACGCGCATTA GACGACGAAC GTTTGTTTTT TTGGTGGCGA TGGTCGCCAC CAAACAAACG GCCTAGTTCT

                                                                           rmaI
                                  bsrI            hinPI                    maeI                 haeIII/palI
                               maeIII     eco57I  hhaI/cfoI                bfaI      bslI      haeI
7201 GCTACCAACT CTTTTTCCGA AGGTAACTGG CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC
     CGATGGTTGA GAAAAAGGCT TCCATTGACC GAAGTCGTCT CGCGTCTATG GTTTATGACA GGAAGATCAC ATCGGCATCA ATCCGGTGGT GAAGTTCTTG

                                                             fnu4HI
                                                             bsoFI                               scrFI
                                                             bbvI                                nciI
                                                         fnu4HI                                  mspI
                                                    alwNI[dcm-]                                  hpaII
                                                   bsrI  bsoFI                                   dsaV      pleI
      scfI    aciI        mnlI             maeIII      bbvI      bsrI                            cauII     hinfI
7301 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT
     AGACATCGTG GCGGATGTAT GGAGCGAGAC GATTAGGACA ATGGTCACCG ACGACGGTCA CCGCTATTCA GCACAGAATG GCCCAACCTG AGTTCTGCTA

                               aciI
                             nspBII                 hgiAI/aspHI
                            fnu4HI                  bsp1286
            mspI            bsoFI                   bsiHKAI
             hpaII          bbvI  mcrI              bmyI
            bsaWI         hinPI   bsiEI             apaLI/snoI
      maeIII              hhaI/cfoI                 alw44I/snoI  aluI                          ddeI      scfI
7401 AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG
     TCAATGGCCT ATTCCGCGTC GCCAGCCCGA CTTGCCCCCC AAGCACGTGT GTCGGGTCGA ACCTCGCTTG CTGGATGTGG CTTGACTCTA TGGATGTCGC
```

FIG. 48W

```
                                                                                                                  scrFI
                                                                                                                  mvaI
                                                                                                                  ecoRII
                                                                      mspI                                        dsaV
             hinPI                                                    hpaII   fnu4HI                  bssSI       bstNI
             hhaI/cfoI                                                bslI    bsoFI                hinPI mnlI     bsaJI
            haeII                                   aciI             bsaWI    aciI                 hhaI/cfoI   aluI apyI[dcm+]
7501 TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA
     ACTCGTAACT CTTTCGCGGT GCGAAGGGCT TCCCTCTTTC CGCCTGTCCA TAGGCCATTC GCCGTCCCAG CCTTGTCCTC TCGCGTGCTC CCTCGAAGGT

         scrFI
         mvaI
         ecoRII
         dsaV
         bstNI                                                            taqI                        nlaIV
         apyI[dcm+]                             mnlI drdI   hgaI             sfaNI              aciI
7601 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA
     CCCCCTTTGC GGACCATAGA AATATCAGGA CAGCCCAAAG CGGTGGAGAC TGAACTCGCA GCTAAAAACA CTACGAGCAG TCCCCCCGCC TCGGATACCT

               haeIII/palI         haeIII/palI
             fnu4HI              scrFI
             bsoFI               mvaI bslI
             aciI                ecoRII
            thaI bslI            dsaV                  nlaIII
            fnuDII/mvnI          bstNI           haeIII/palI  nspI
            bstUI                apyI[dcm+]      haeI         nspHI                     tfiI
      cac8I bsh1236I       nlaIV  haeI        cac8I           aflIII                    hinfI
7701 AAAACGCCAG CAACGCGGCC TTTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC TGCGTTATCC CCTGATTCTG TGGATAACCG
     TTTTGCGGTC GTTGCGCCGG AAAAATGCCA AGGACCGGAA AACGACCGGA AAACGAGTGT ACAAGAAAGG ACGCAATAGG GGACTAAGAC ACCTATTGGC

                                   fnu4HI
                                   bsoFI                 fnu4HI
                                   bbvI                  bsoFI                       sapI  hinPI
                               cac8I aciI                bbvI pleI                   mboII hhaI/cfoI
                             bsrBI  fnu4HI       mcrI   hinPI  hinfI                 earI/ksp632I
      aciI           aluI    aciI   bsoFI       bsiEI   hhaI/cfoI            mnlI  aciI   haeII
7801 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA
     ATAATGGCGG AAACTCACTC GACTATGGCG AGCGGCGTCG GCTTGCTGGC TCGCGTCGCT CAGTCACTCG CTCCTTCGCC TTCTCGCGGG TTATGCGTTT
```

FIG. 48X

```
                 thaI
                 fnuDII/mvnI
                 bstUI
                 bsh1236I
                hinPI
                hhaI/cfoI
               thaI
               fnuDII/mvnI                 cac8I
               bstUI   haeIII/palI        aluI
               bsh1236I         tru9I   pvuII                                              tru9I
      mnlI     bslI    eaeI  tfiI aseI/asnI/vspI                          cac8I       hinPI       mseI      maeIII
    aciI       aciI    cfrI  hinfI mseI   nspBII                  bsrI      aciI        hhaI/cfoI  aseI/asnI/vspI
7901 CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATCCAGCT GGCACGACAG GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT
     GGCGGAGAGG GGCGCGCAAC CGGCTAAGTA ATTAGGTCGA CCGTGCTGTC CAAAGGGCTG ACCTTTCGCC CGTCACTCGC GTTGCGTTAA TTACACTCAA

                       scrFI
                       mvaI
                       ecoRII
                       dsaV
                 nlaIV bstNI
                 hgiCI apyI[dcm+]           mspI                      aciI
      mnlI       banI bsaJI                 hpaII                    bsrBI                          aluI
8001 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA
     TGGAGTGAGT AATCCGTGGG GTCCGAAATG TGAAATACGA AGGCCGAGCA TACAACACAC CTTAACACTC GCCTATTGTT AAAGTGTGTC CTTTGTCGAT
```

FIG. 48Y

```
                      tru9I
                      mseI
                     aseI/asnI/vspI
                    xmnI
          nlaIII    asp700
  8101 TGACCATGAT TACGAATTAA  (SEQ ID NO.68)
       ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC):          1690 5947
acc65I(GGTACC):         2969 3967 4529
accI(GTMKAC):           823 1039 2738 4237
aciI(CCGC):             217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
                        3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
                        4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
                        5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
                        7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070
acyI                    see hinlI
aflII/bfrI(CTTAAG):     786
aflIII(ACRYGT):         932 7758
ageI(ACCGGT):           1833
ahaII/bsaHI(GRCGYC):    988 1690 1858 5117 5947 6329
ahaIII/draI(TTTAAA):    696 4935 6290 6982 7001
ahdI/eam1105I(GACNNNNNGTC): 2087 6865
aluI(AGCT):             5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
                        3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
                        5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
alw44I/snoI(GTGCAC):    1876 5651 6198 7444
```

FIG. 48Z

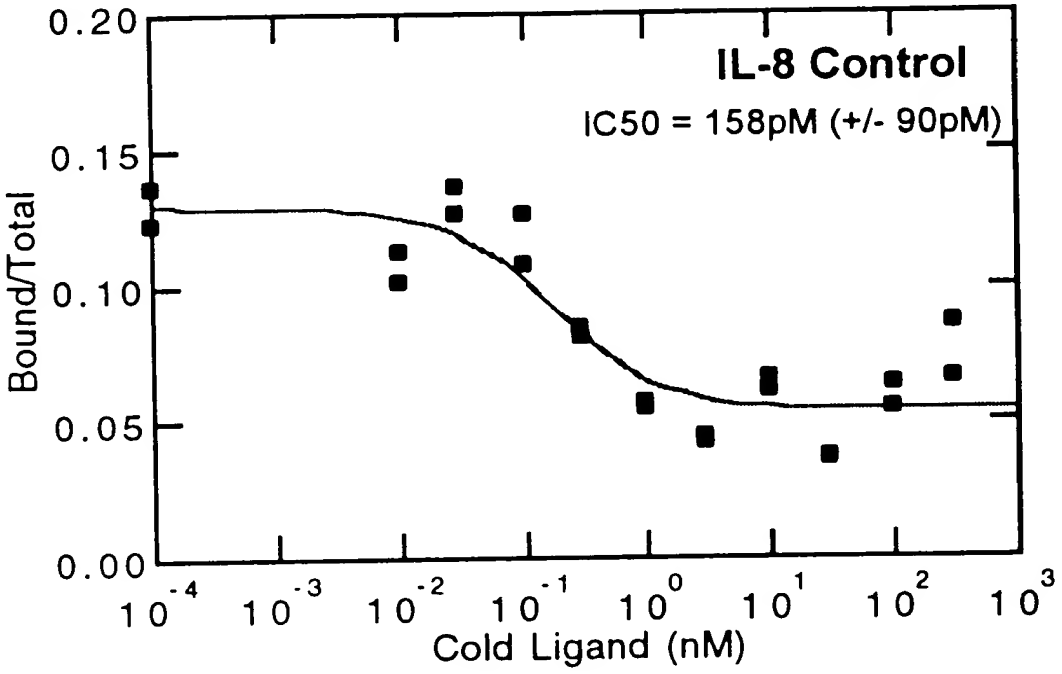


FIG. 49A

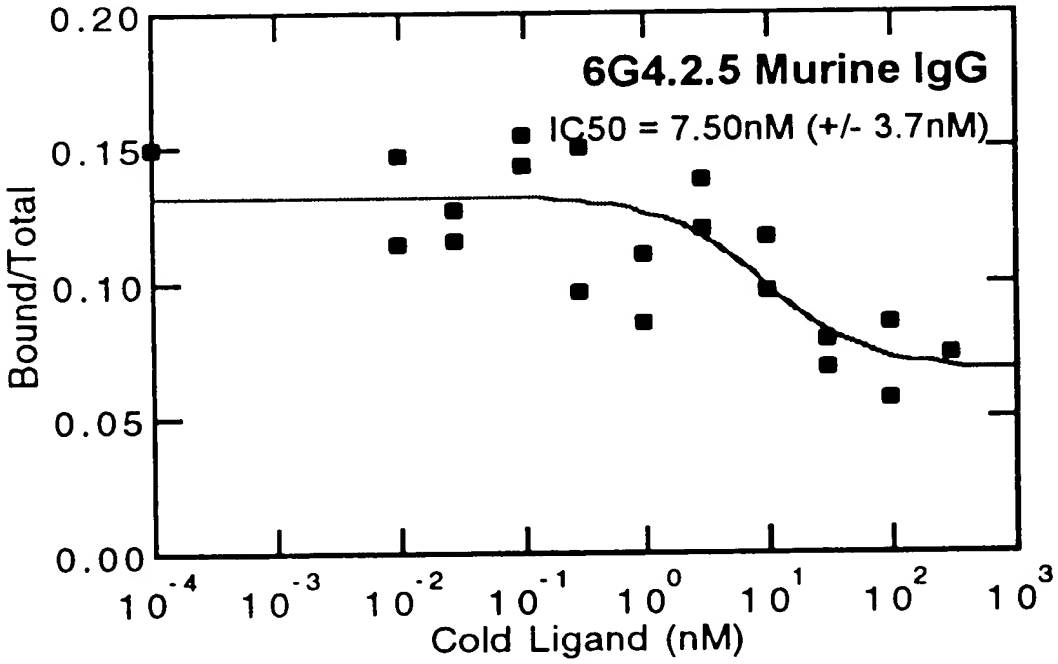


FIG. 49B

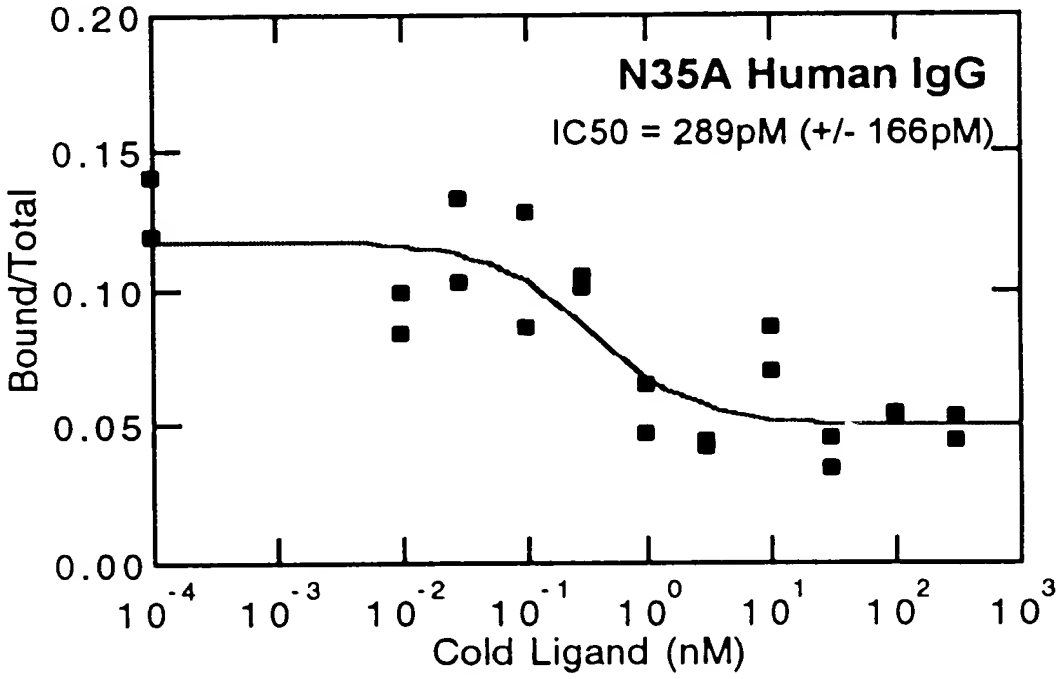


FIG. 49C

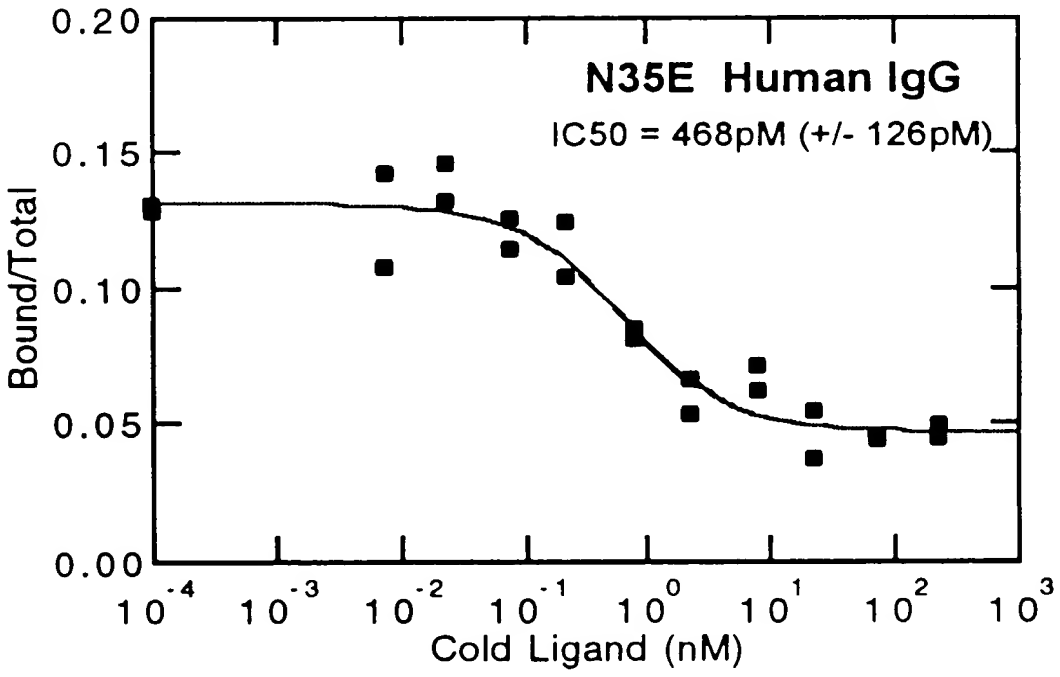


FIG. 49D

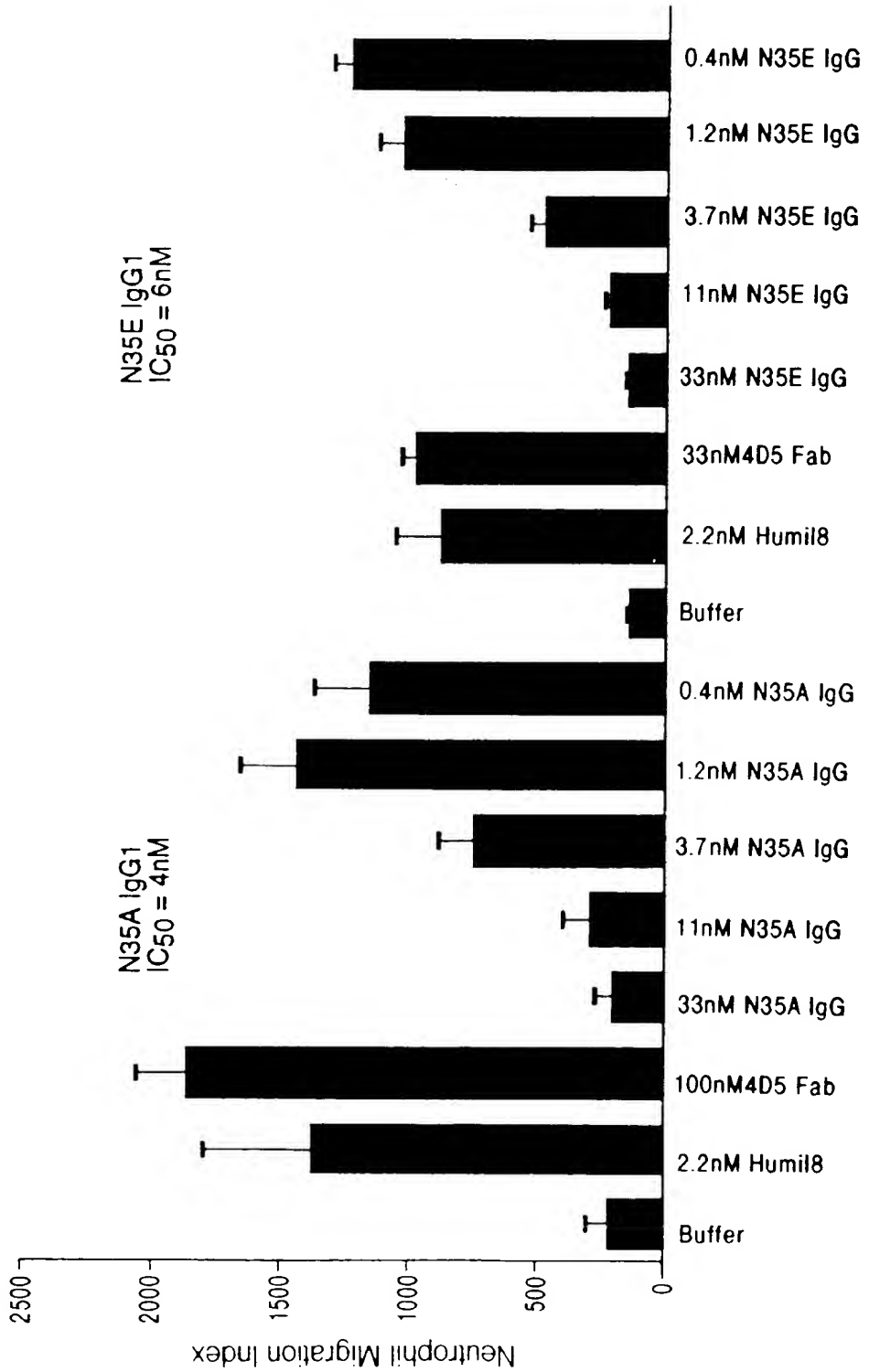


FIG. 50A

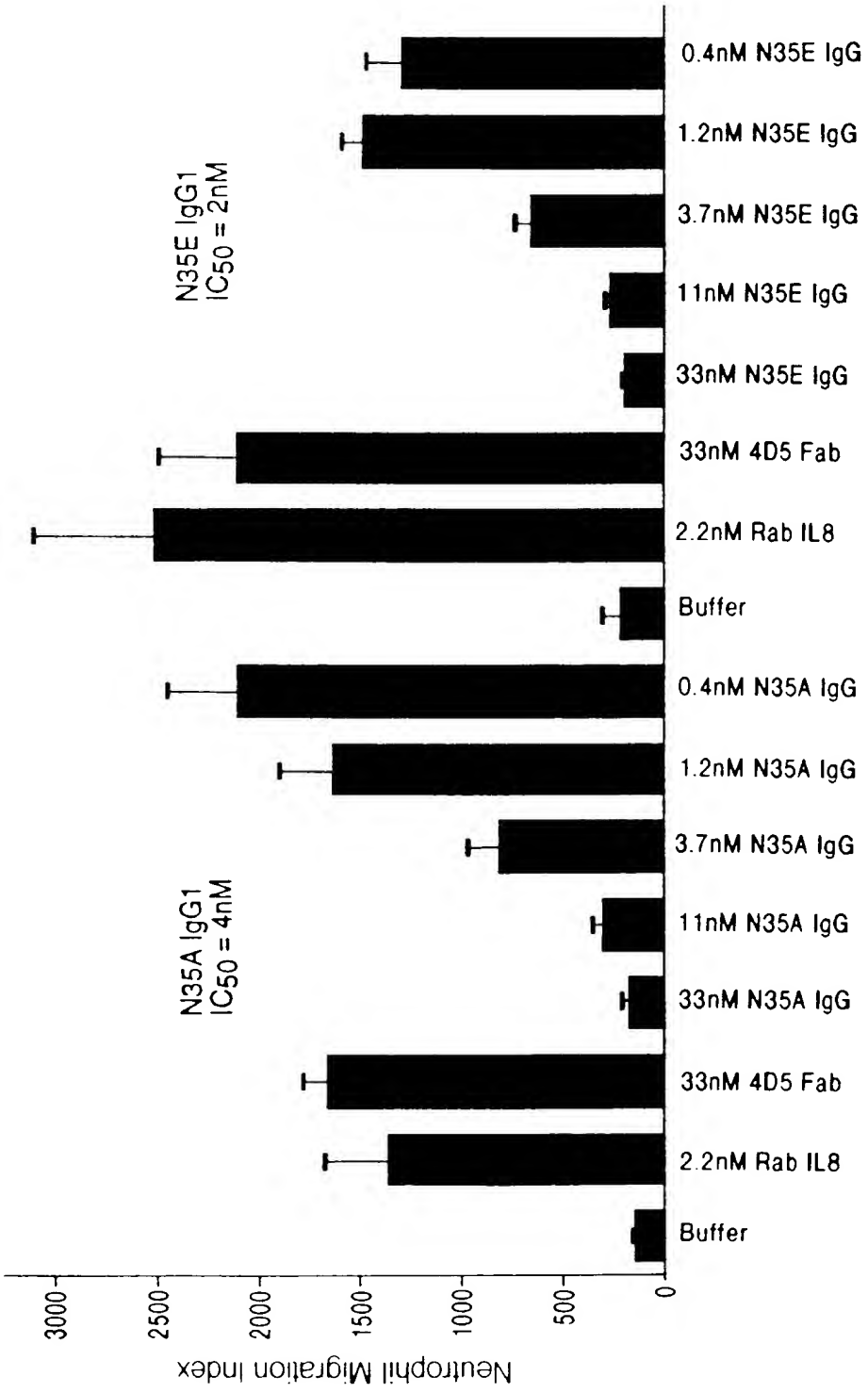
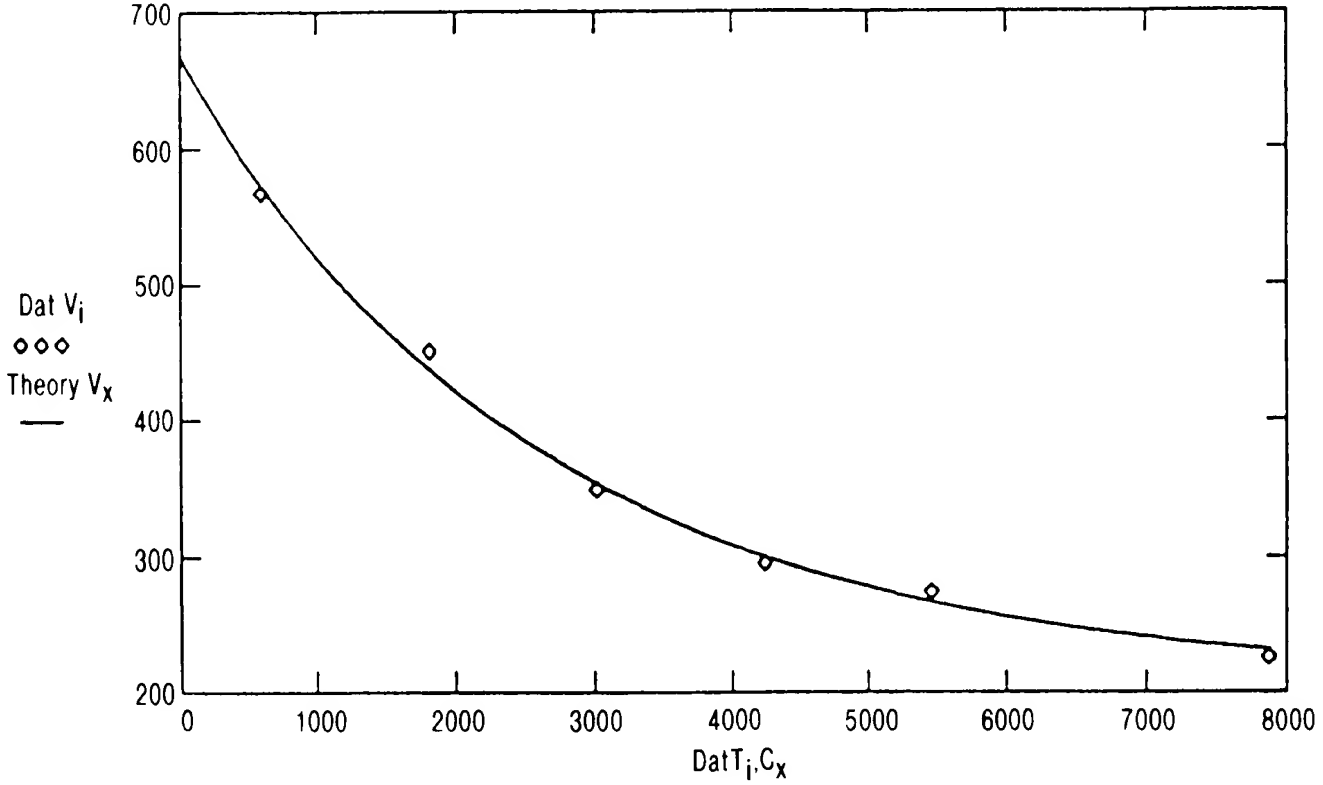


FIG. 50B



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.IgG1

SAMPLE	ka	kd	Kd
Murine 6G4.2.5 IgG2a	$8.3x10^5$	$2.9x10^{-4}$	350pM
6G4V11N35A-IgG1	$8.7x10^5$	$7.7x10^{-5}$	88pM
6G4V11N35E-IgG1	$3.0x10^6$	$1.4x10^{-4}$	49pM

FIG. 51

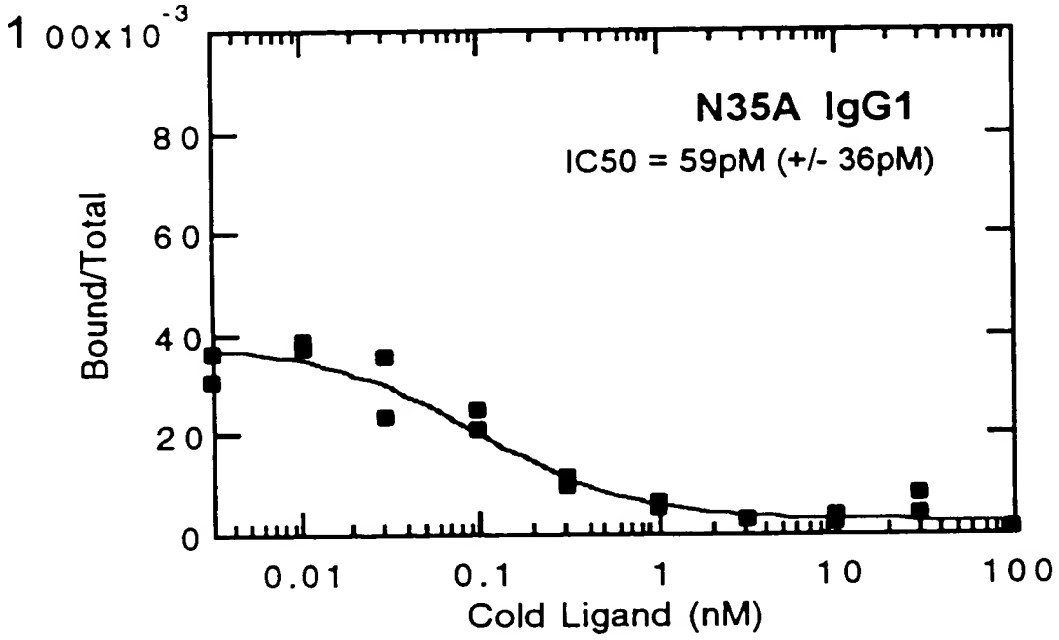


FIG. 52A

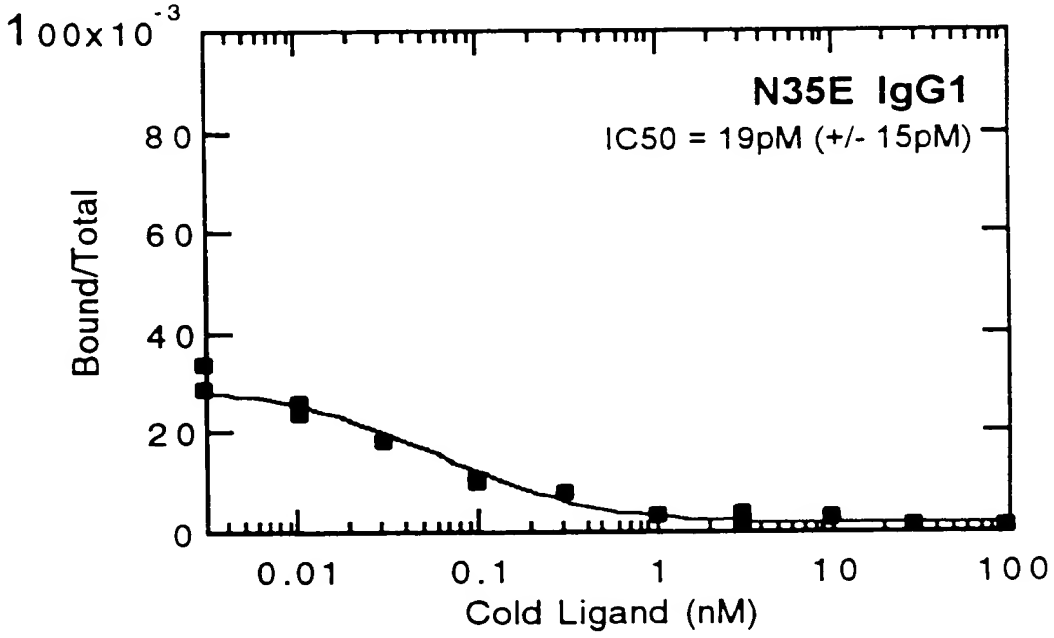


FIG. 52B

```
781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
    TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT
 -1                                   M  K  K  N     I  A  F     L  L  A

841 TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT
    AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S  M  F  V     F  S  I     A  T  N     A  Y  A  E     V  Q  L     V  Q  S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
    CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
  8 G  G  G  L     V  Q  P     G  G  S     L  R  L  S     C  A  A     S  G  Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
    AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
 28 S  F  S  S     H  Y  M     H  W  V     R  Q  A  P     G  K  G     L  E  W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
     CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
  48 V  G  Y  I     D  P  S     N  G  E     T  T  Y  N     Q  K  F     K  G  R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
     AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
  68 F  T  L  S     R  D  N     S  K  N     T  A  Y  L     Q  M  N     S  L  R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
     CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
  88 A  E  D  T     A  V  Y     Y  C  A     R  G  D  Y     R  Y  N     G  D  W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
     AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
 108 F  F  D  V     W  G  Q     G  T  L     V  T  V  S     S  A  S     T  K  G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
     GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCCGTG TCGCCGGGAC
 128 P  S  V  F     P  L  A     P  S  S     K  S  T  S     G  G  T     A  A  L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
     CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
 148 G  C  L  V     K  D  Y     F  P  E     P  V  T  V     S  W  N     S  G  A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
     GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
 168 L  T  S  G     V  H  T     F  P  A     V  L  Q  S     S  G  L     Y  S  L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
     TCGTCGCACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC
 188 S  S  V  V     T  V  P     S  S  S     L  G  T  Q     T  Y  I     C  N  V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
     TTAGTGTTCG GGTCGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
 208 N  H  K  P     S  N  T     K  V  D     K  K  V  E     P  K  S     C  D  K

1561 ACTCACACAT GCCCGCCGTGA  (SEQ ID NO.69)
     TGAGTGTGTA CGGGCGGCACT
 228 T  H  T  C     P  P  O     (SEQ ID NO.70)
```

FIG. 53

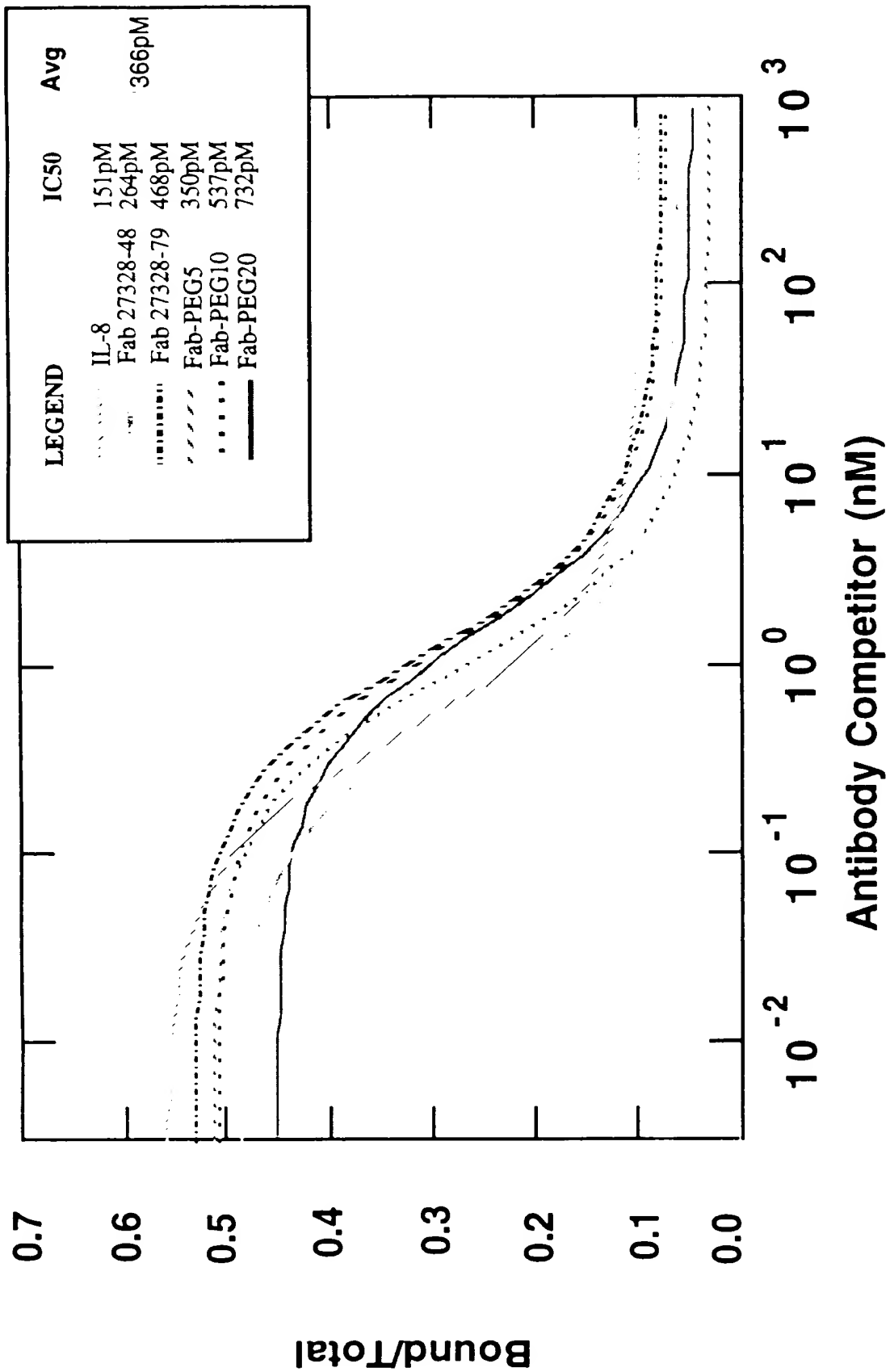


FIG. 54A

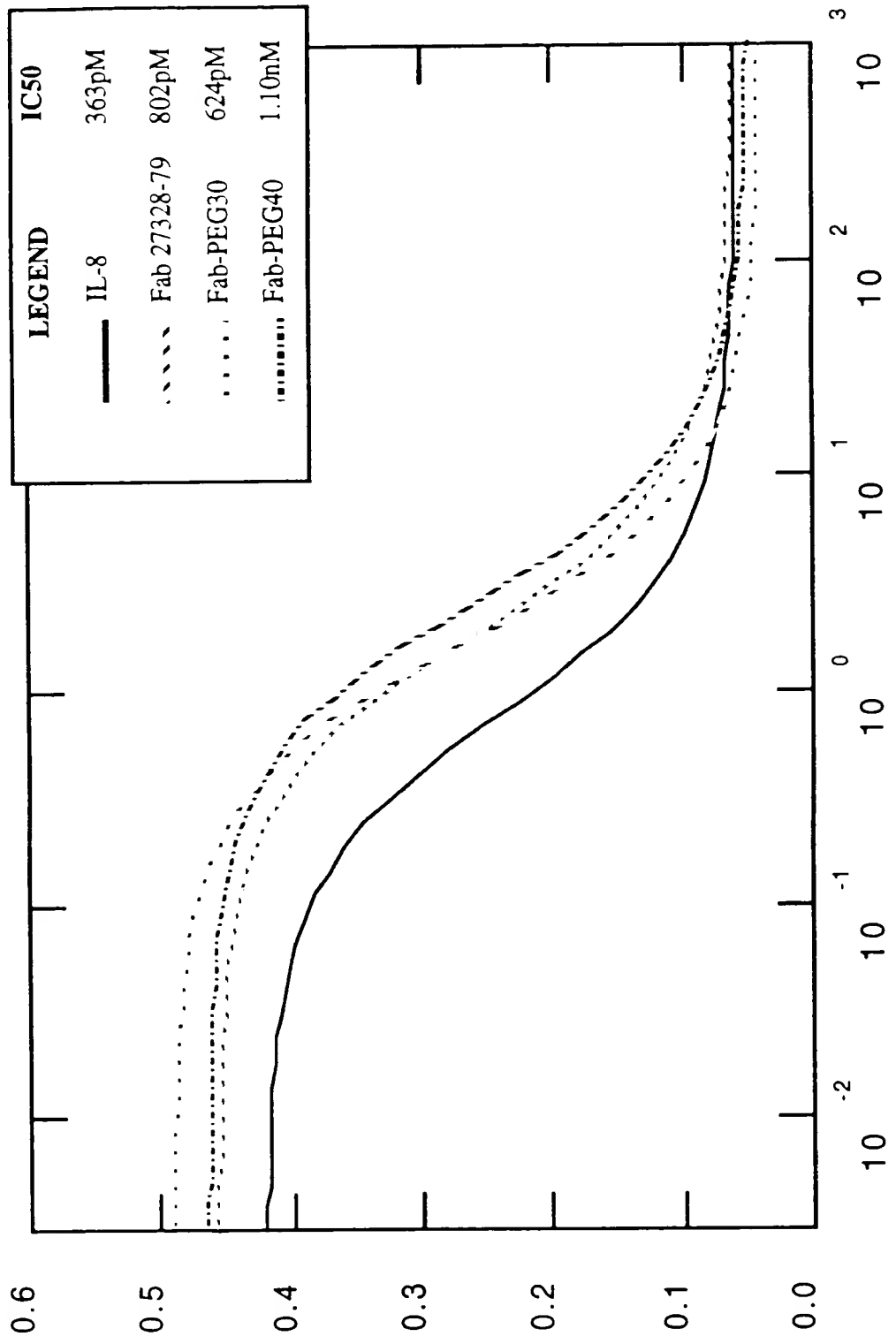


FIG. 54B

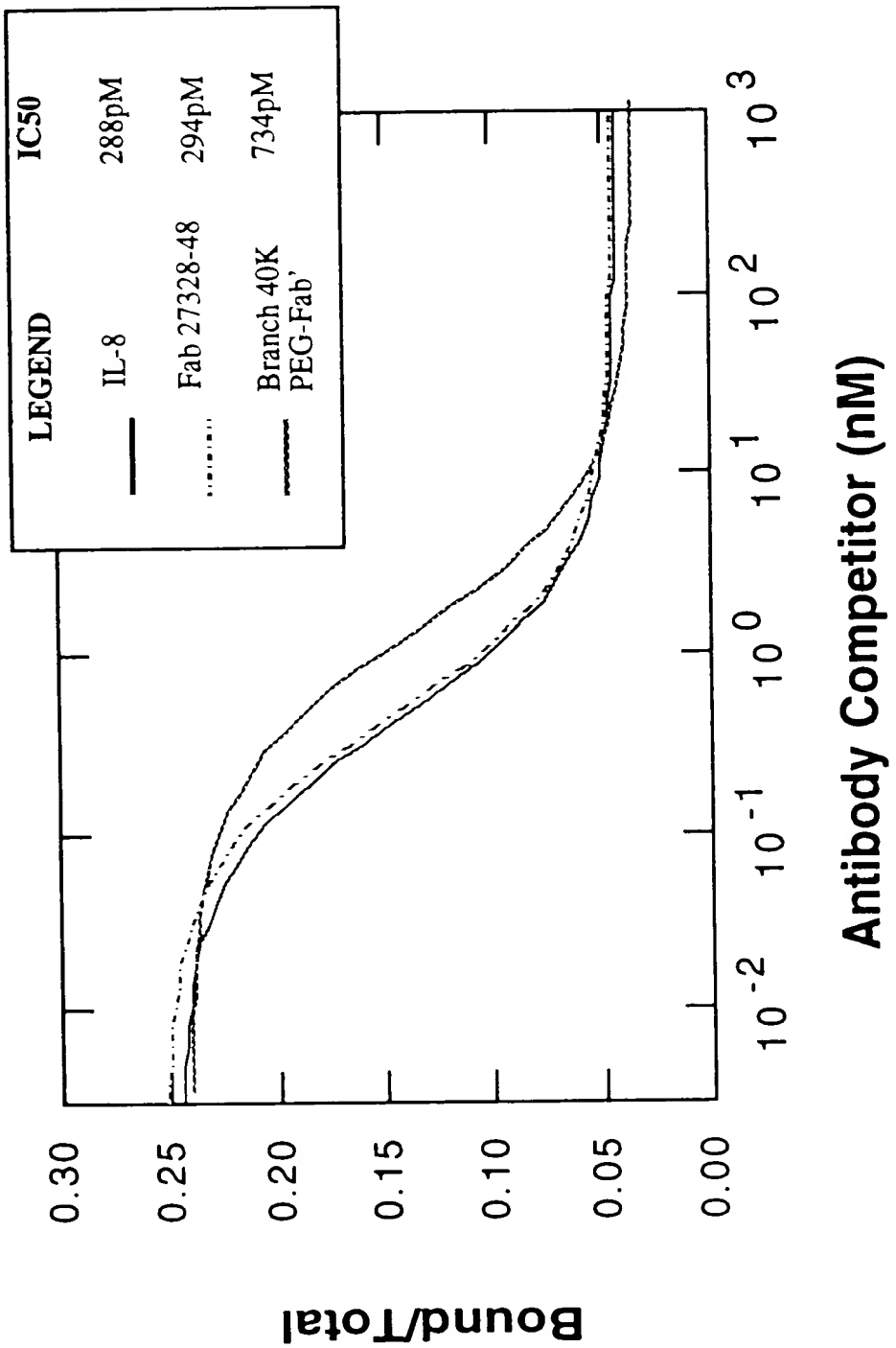


FIG. 54C

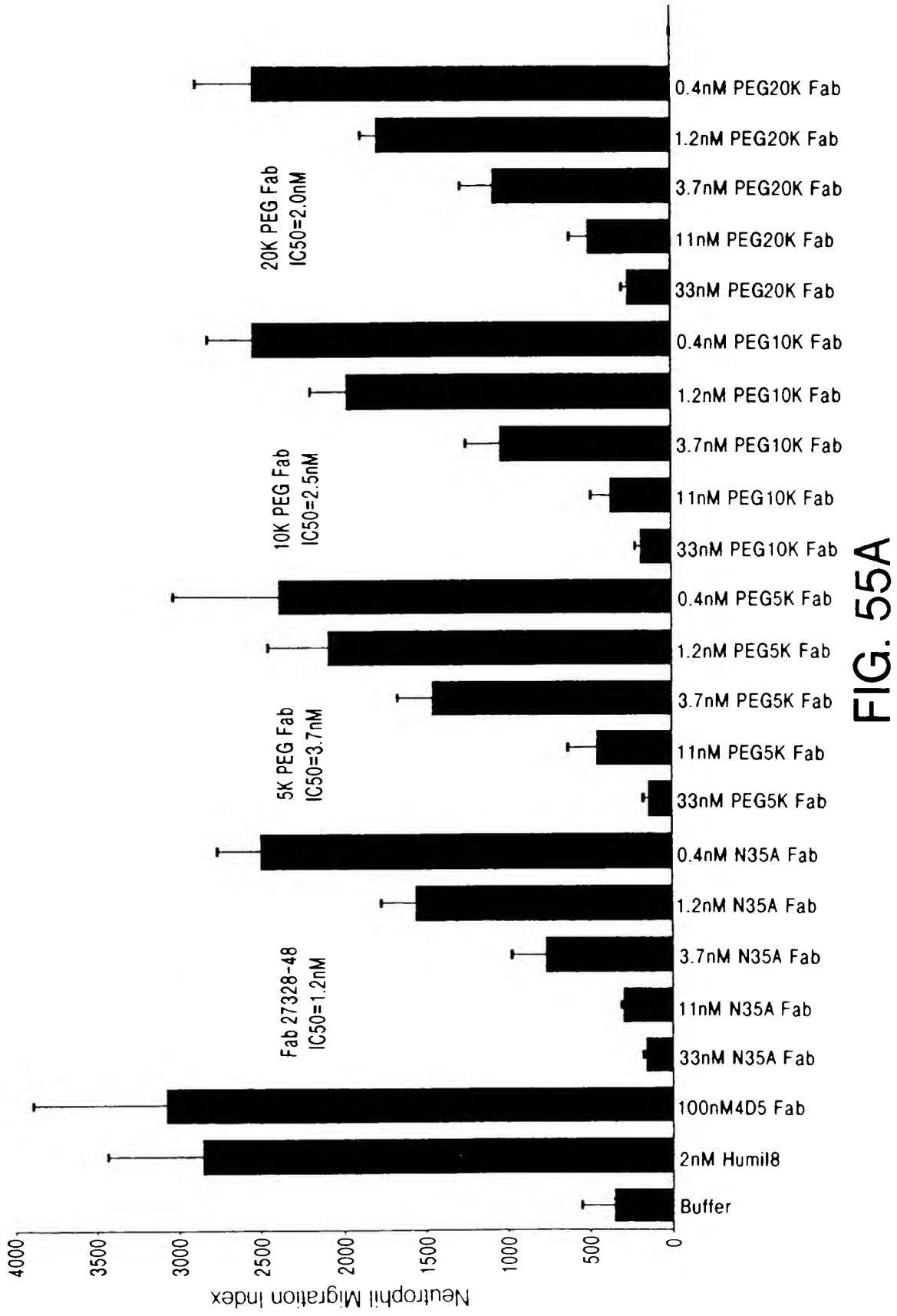


FIG. 55A

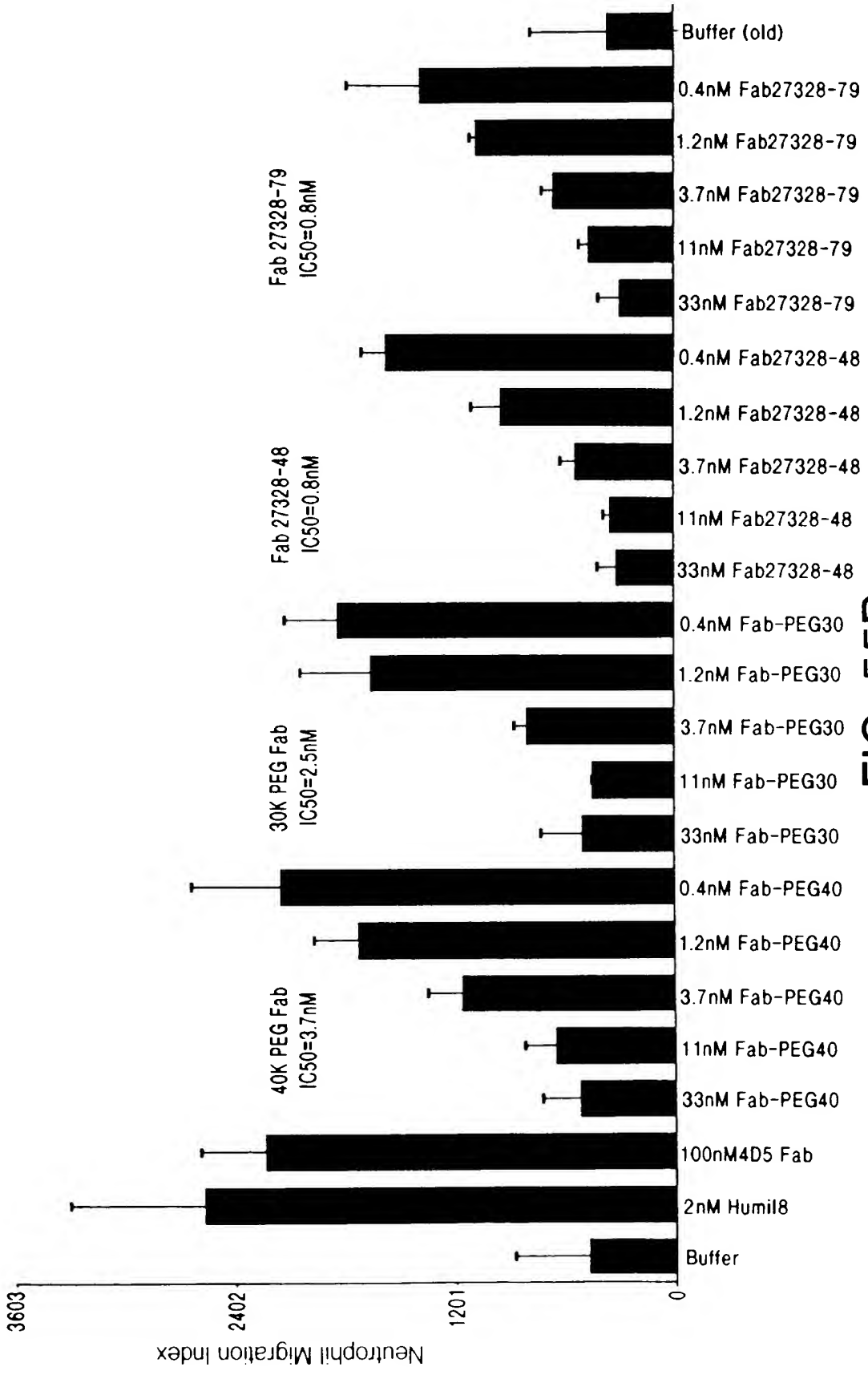


FIG. 55B

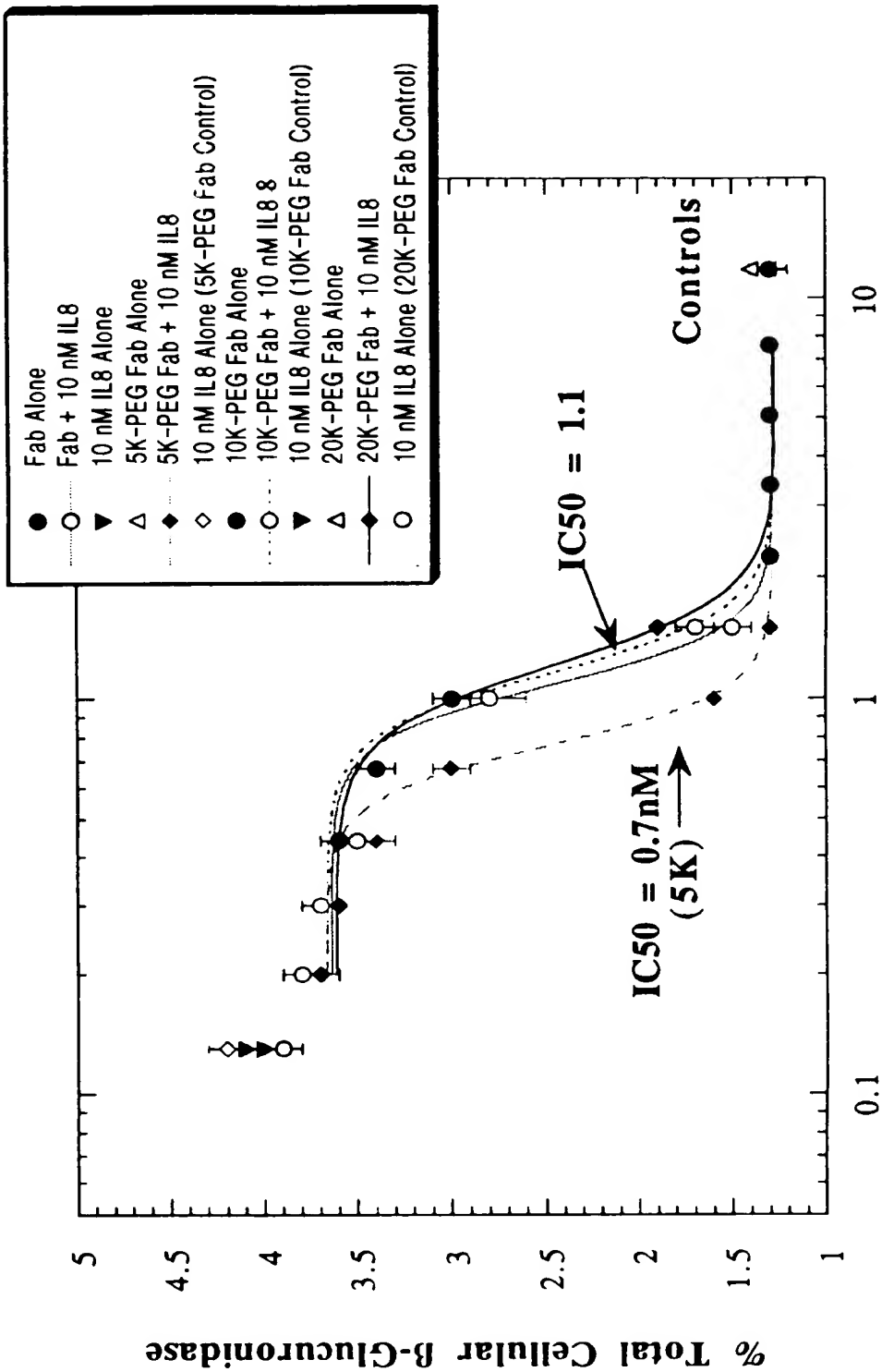

Fab Alone
Fab + 10 nM IL8
10 nM IL8 Alone
5K-PEG Fab Alone
5K-PEG Fab + 10 nM IL8
10 nM IL8 Alone (5K-PEG Fab Control)
10K-PEG Fab Alone
10K-PEG Fab + 10 nM IL8 8
10 nM IL8 Alone (10K-PEG Fab Control)
20K-PEG Fab Alone
20K-PEG Fab + 10 nM IL8
10 nM IL8 Alone (20K-PEG Fab Control)
IC50 = 1.1
Controls
IC50 = 0.7nM
(5K)
% Total Cellular β-Glucuronidase
Molar Ratio Antibody:IL-8
5
4.5
4
3.5
3
2.5
2
1.5
1
0.1
1
10

FIG. 56A

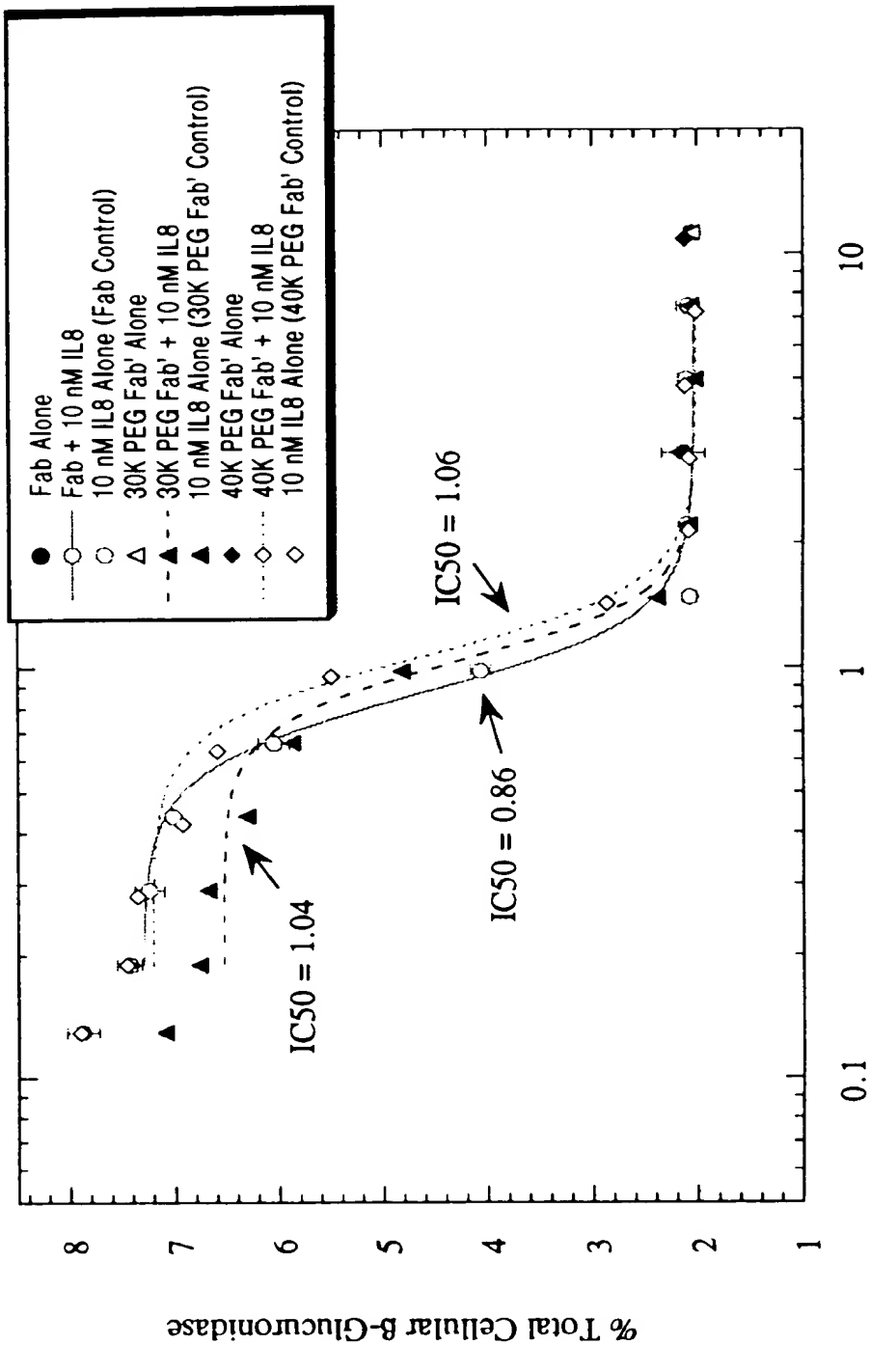


FIG. 56B

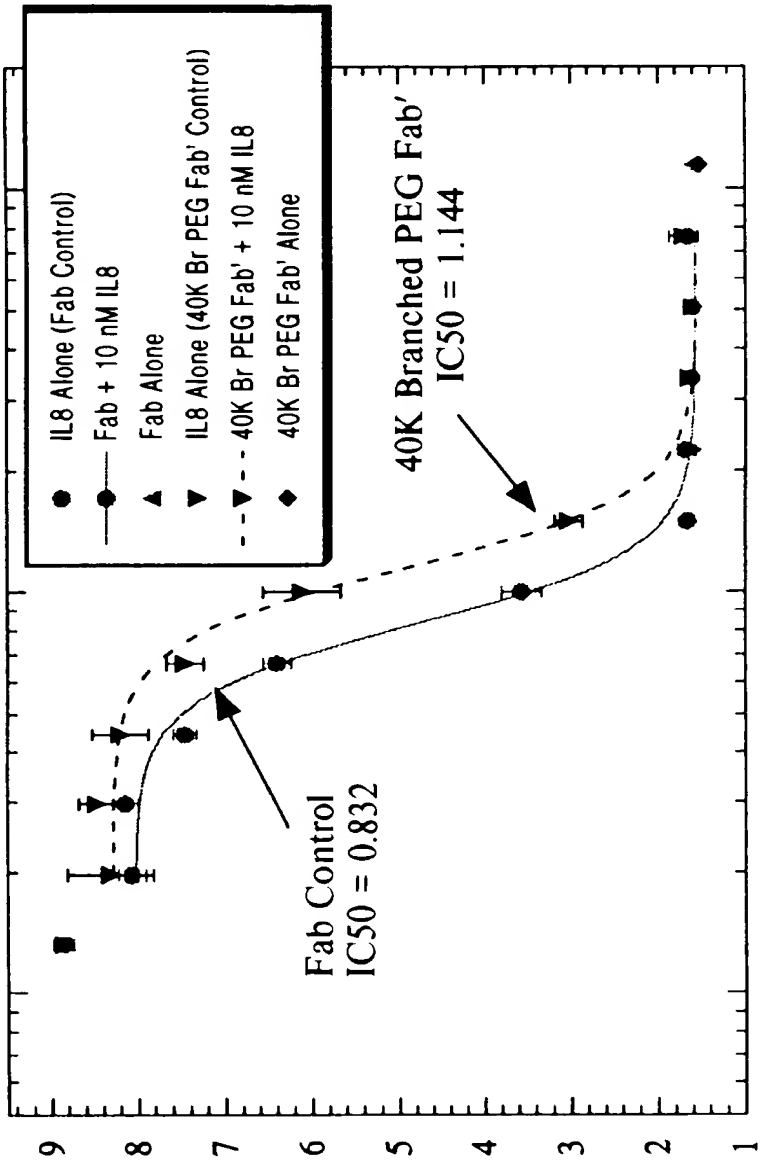


FIG. 56C

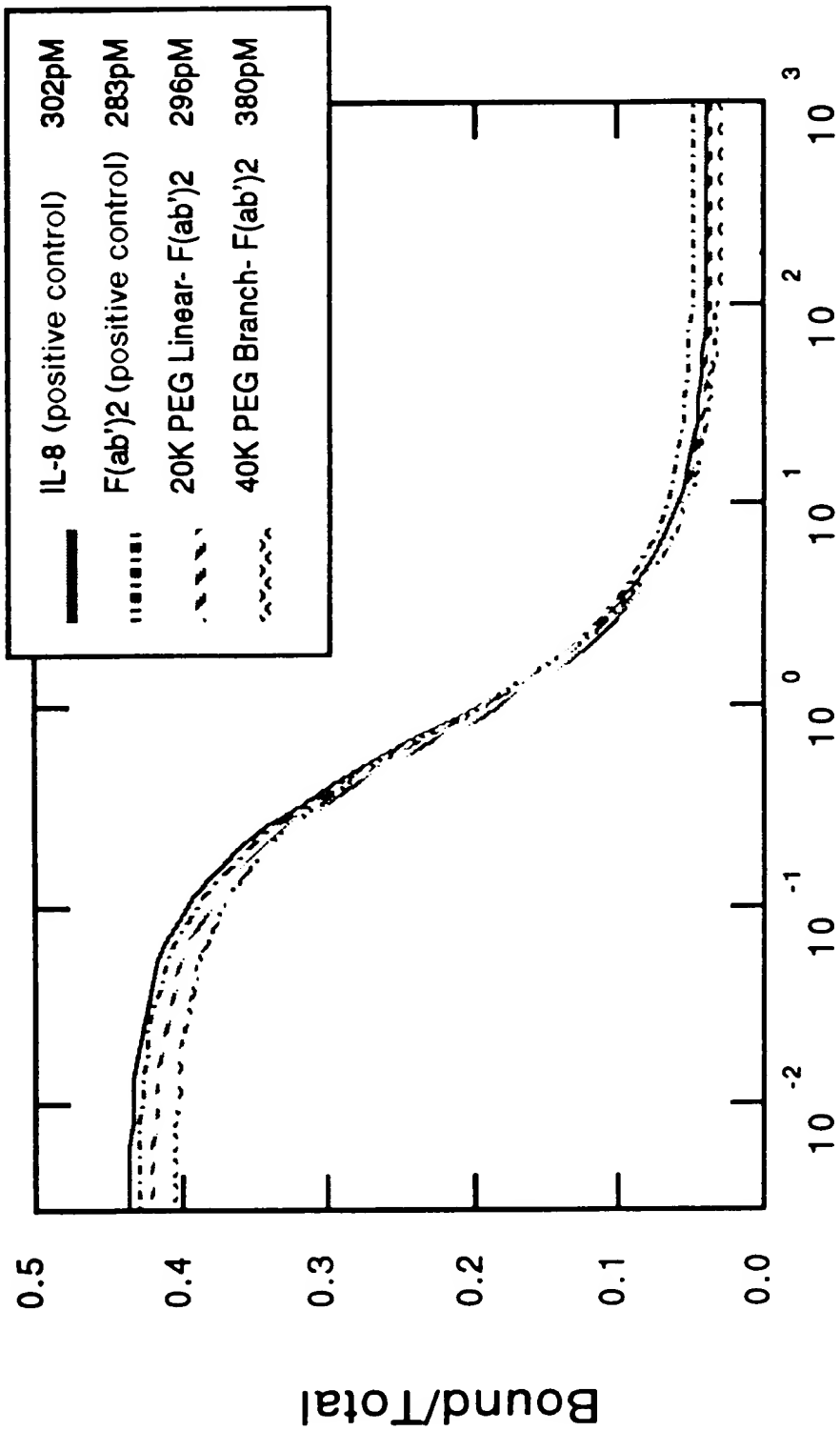


FIG. 57A

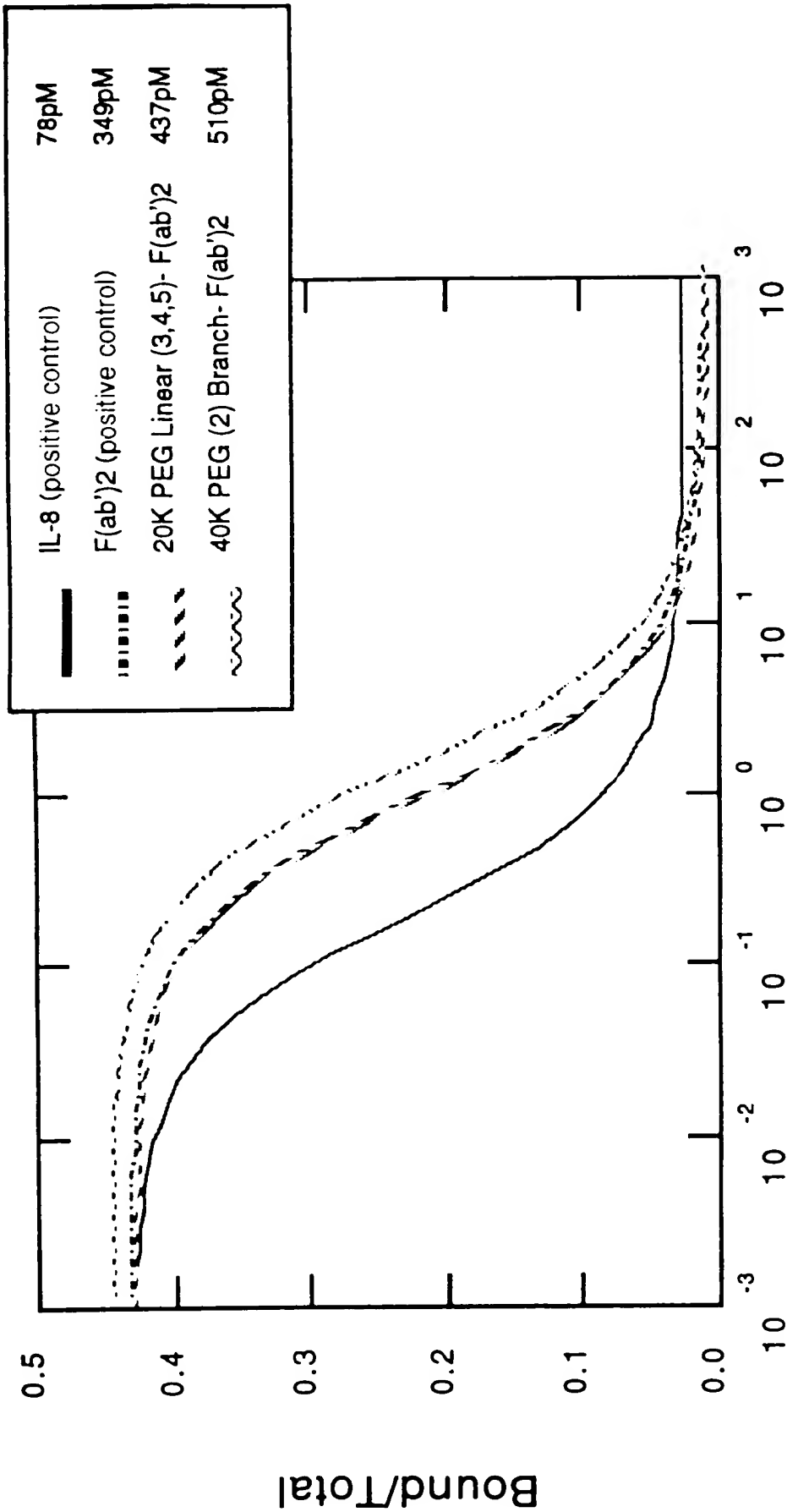


FIG. 57B

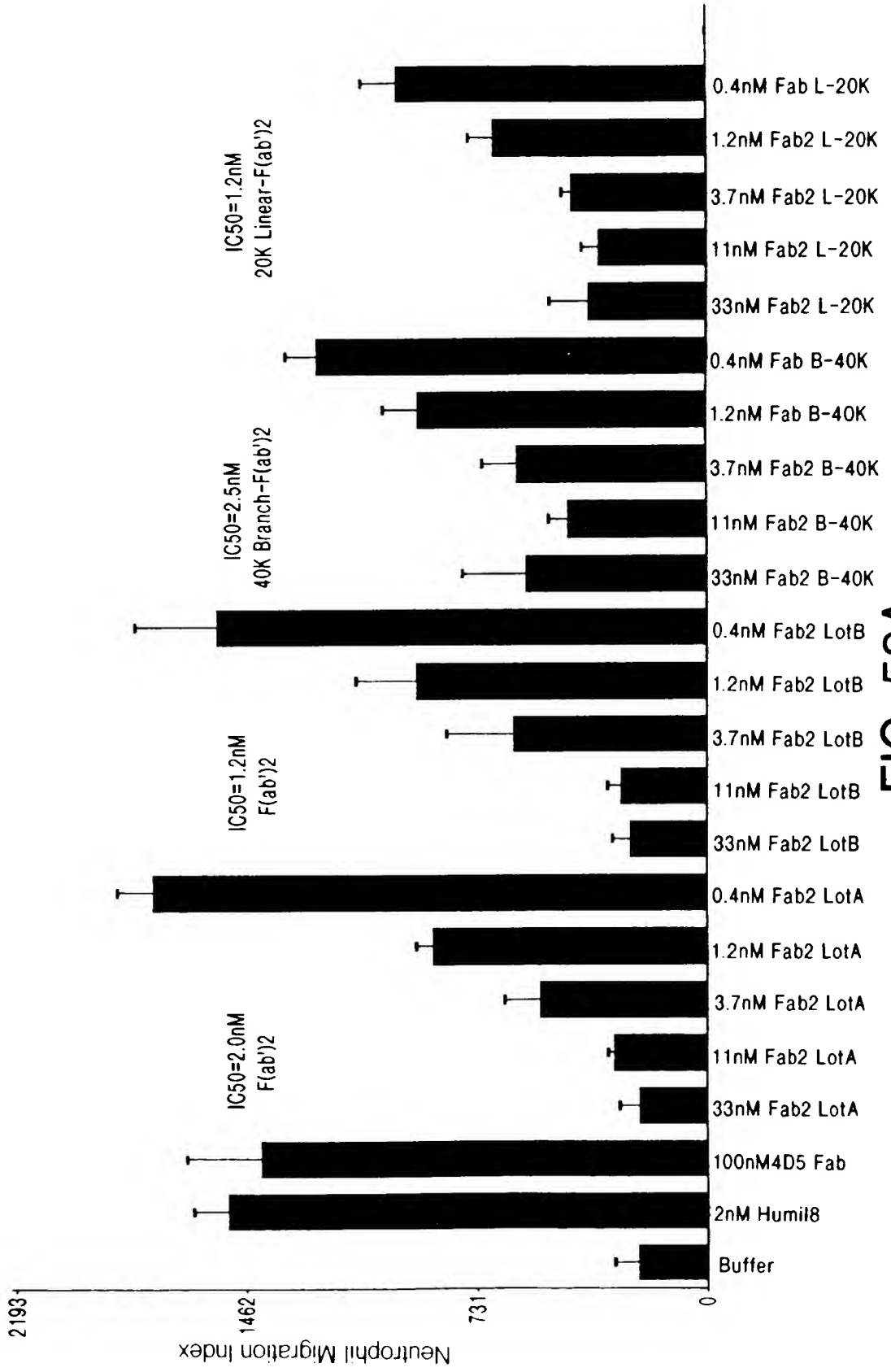


FIG. 58A

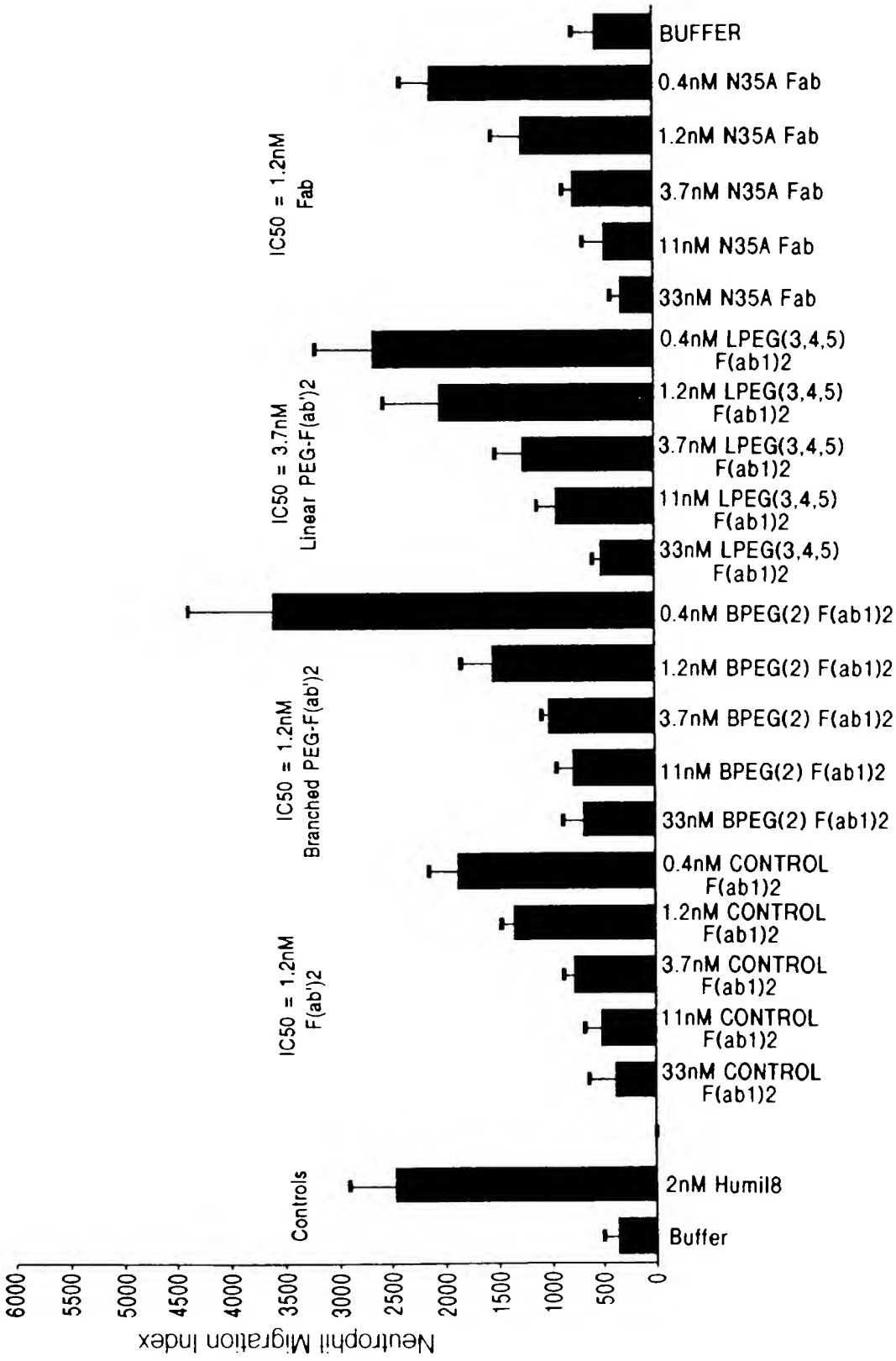


FIG. 58B

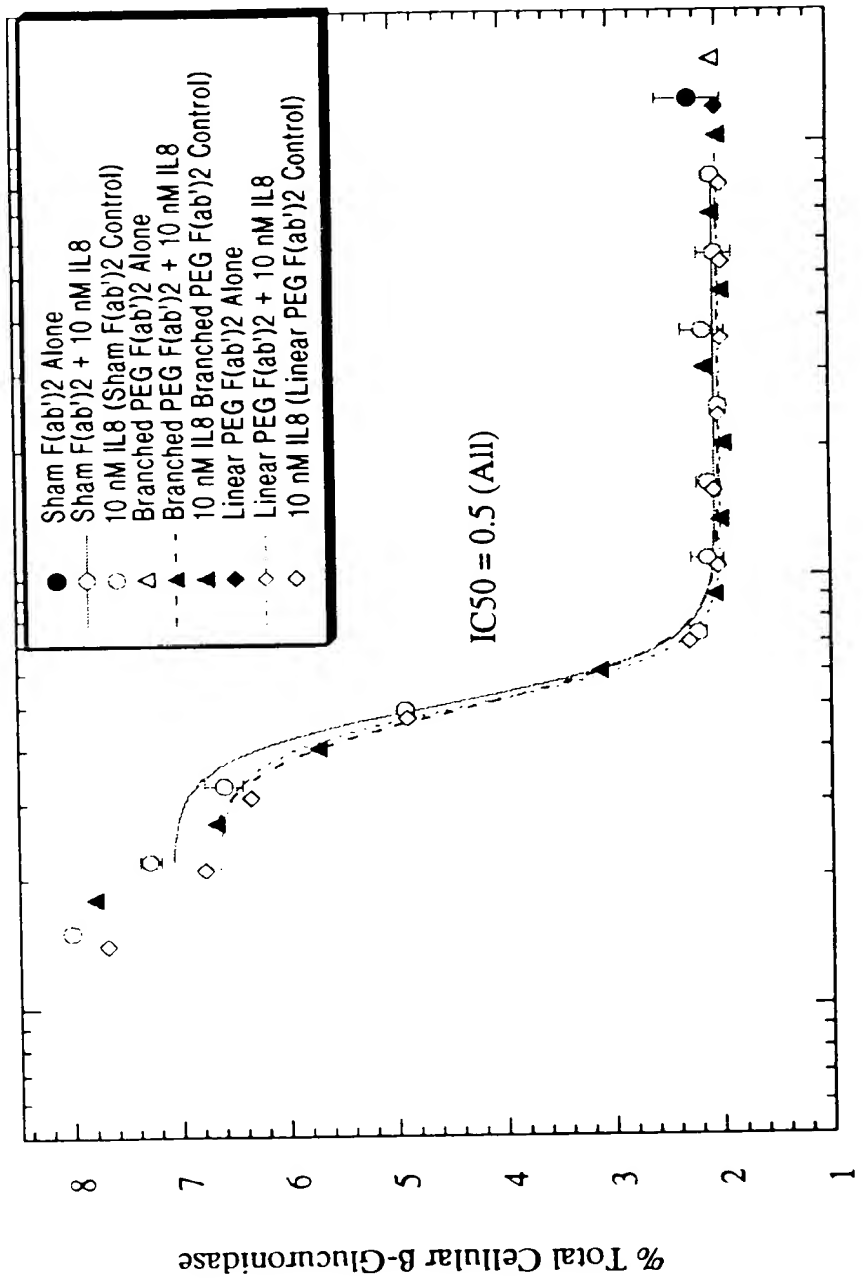


FIG. 59A

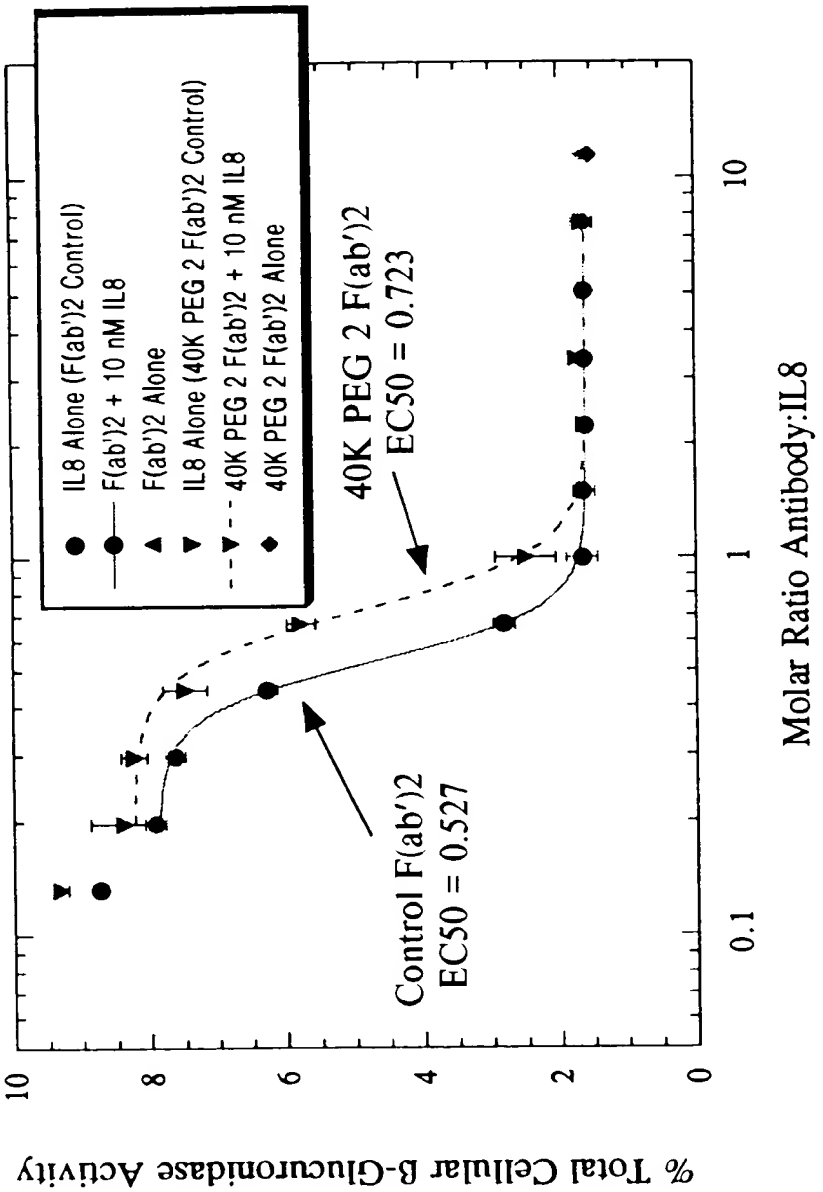


FIG. 59B

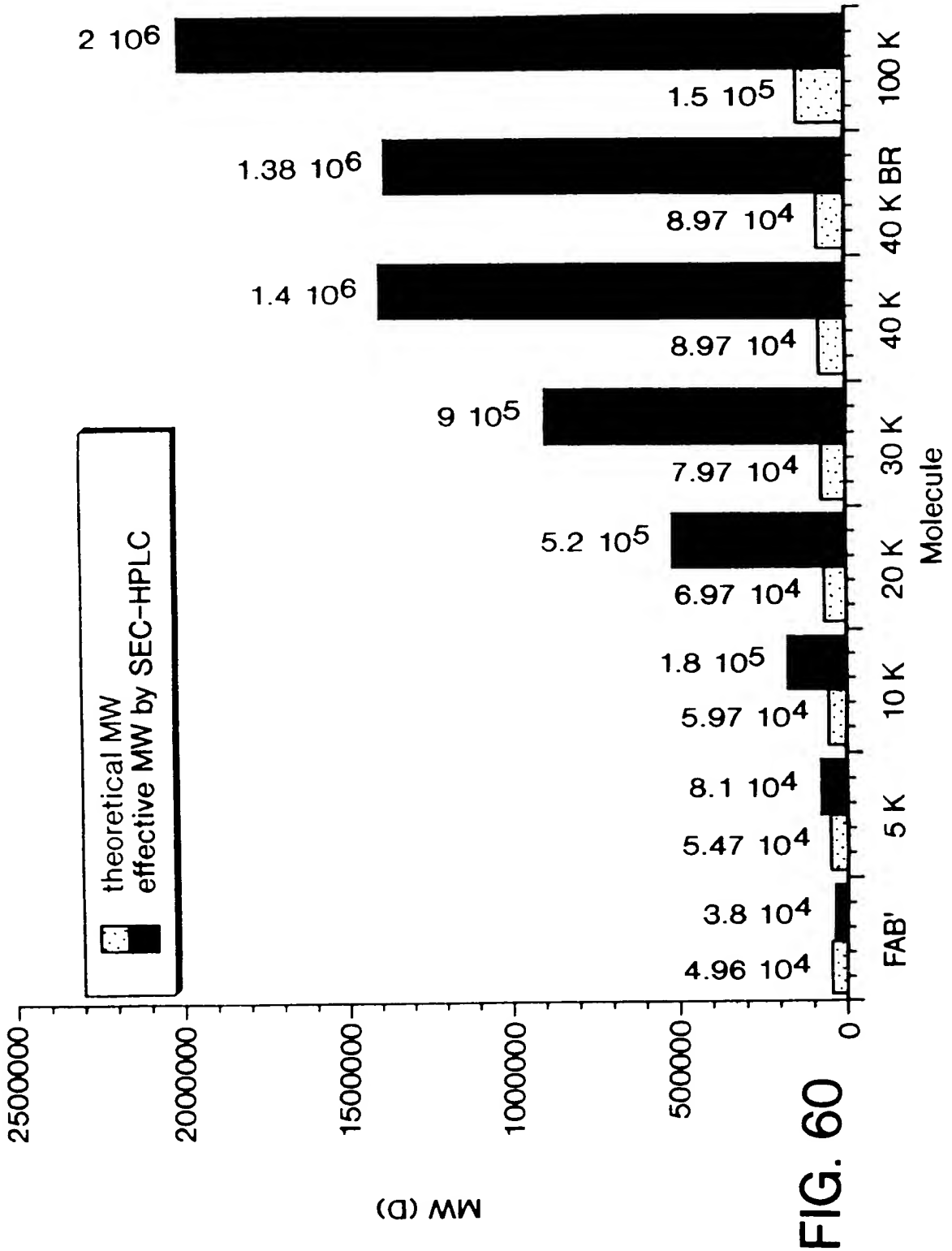


FIG. 60

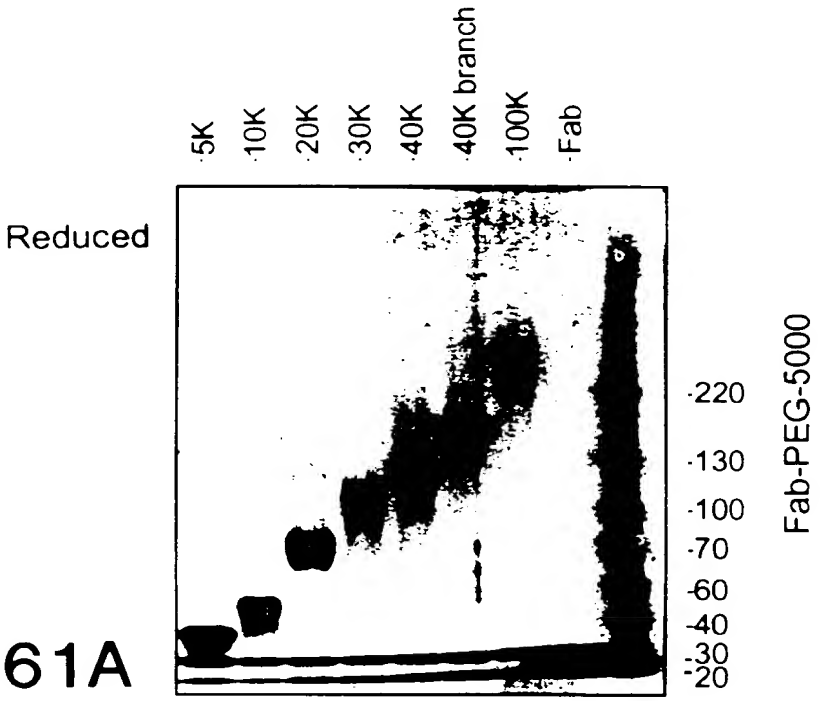


FIG. 61A

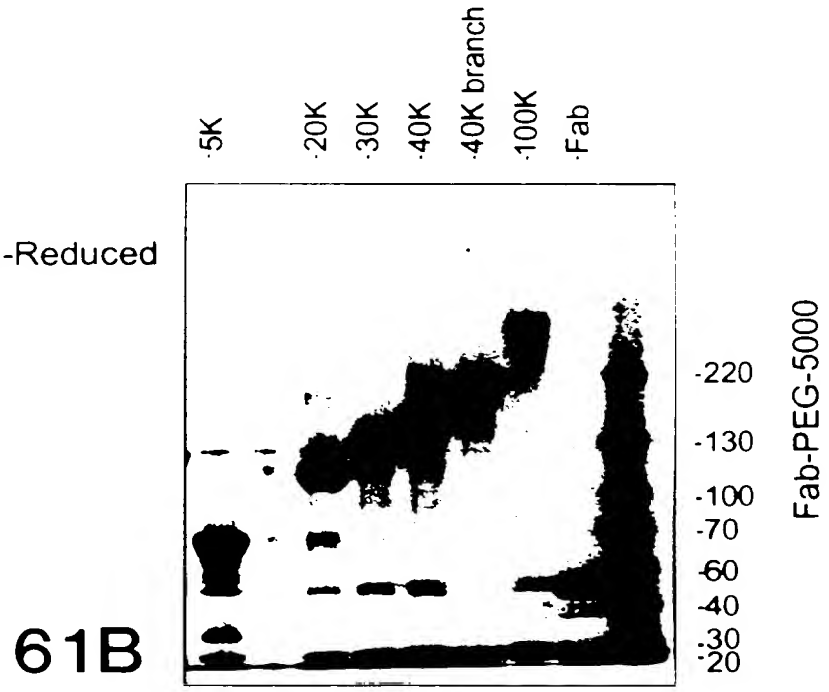


FIG. 61B

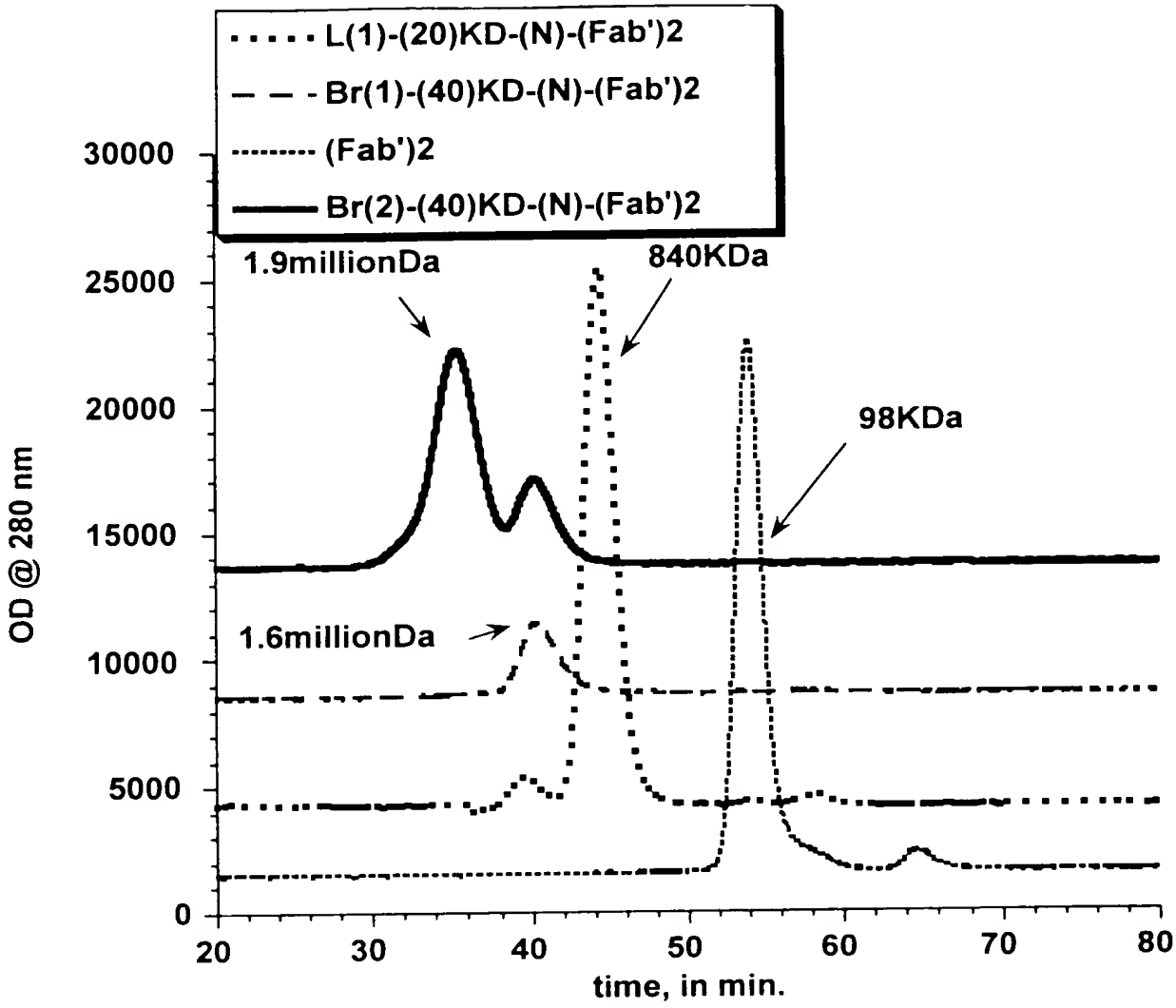


FIG. 62

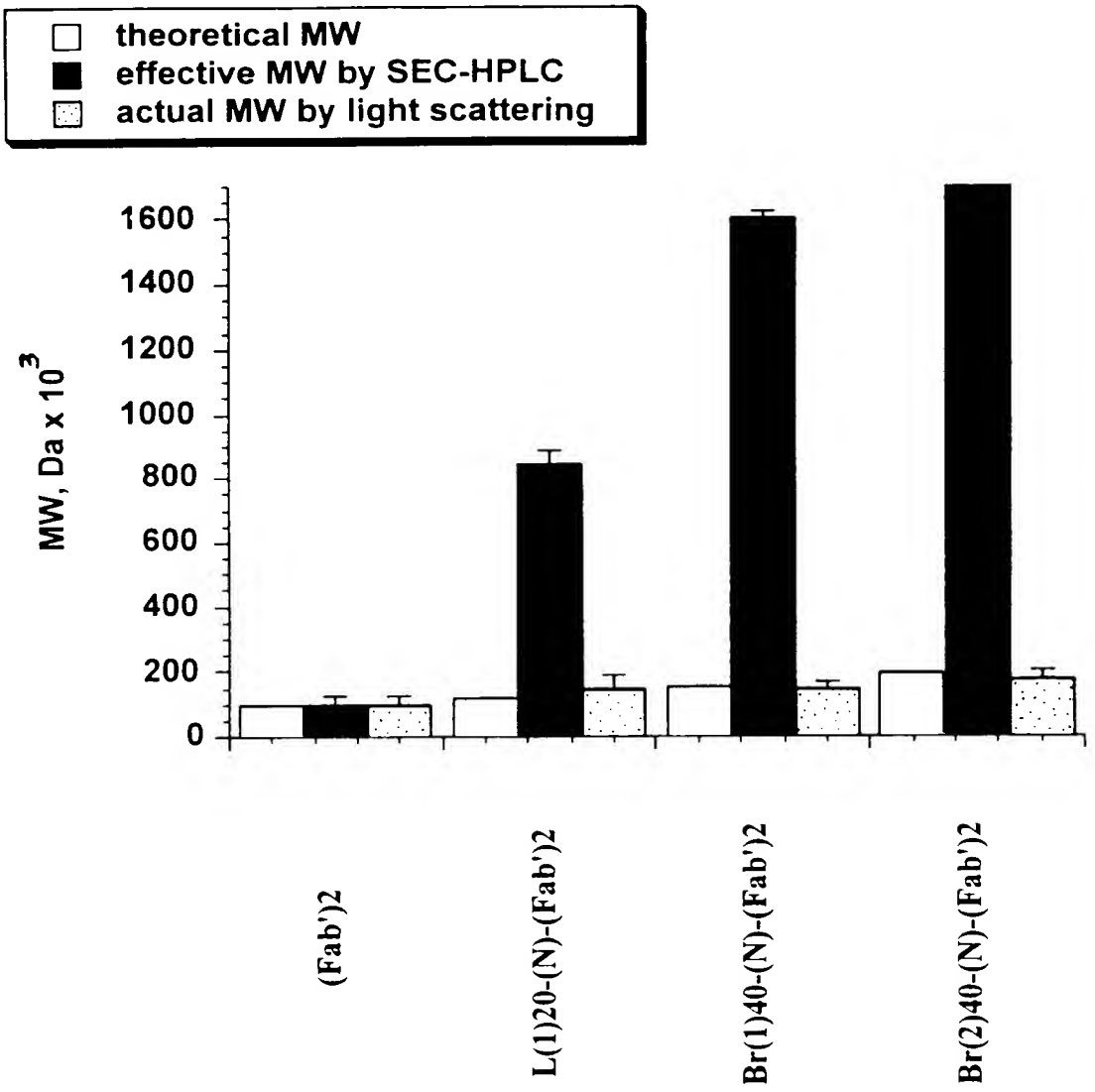


FIG. 63

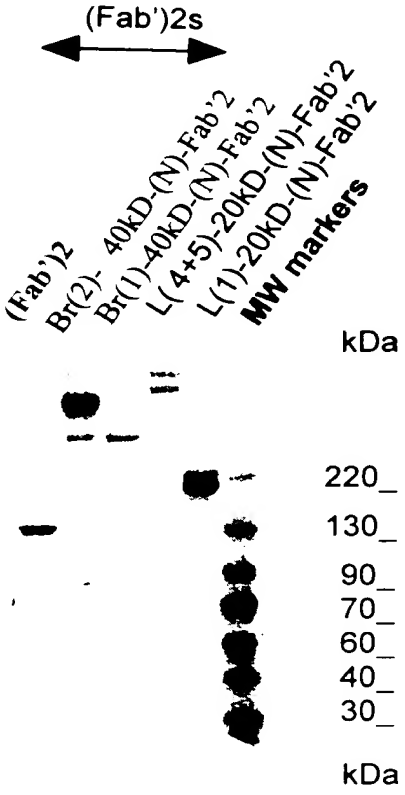


FIG. 64

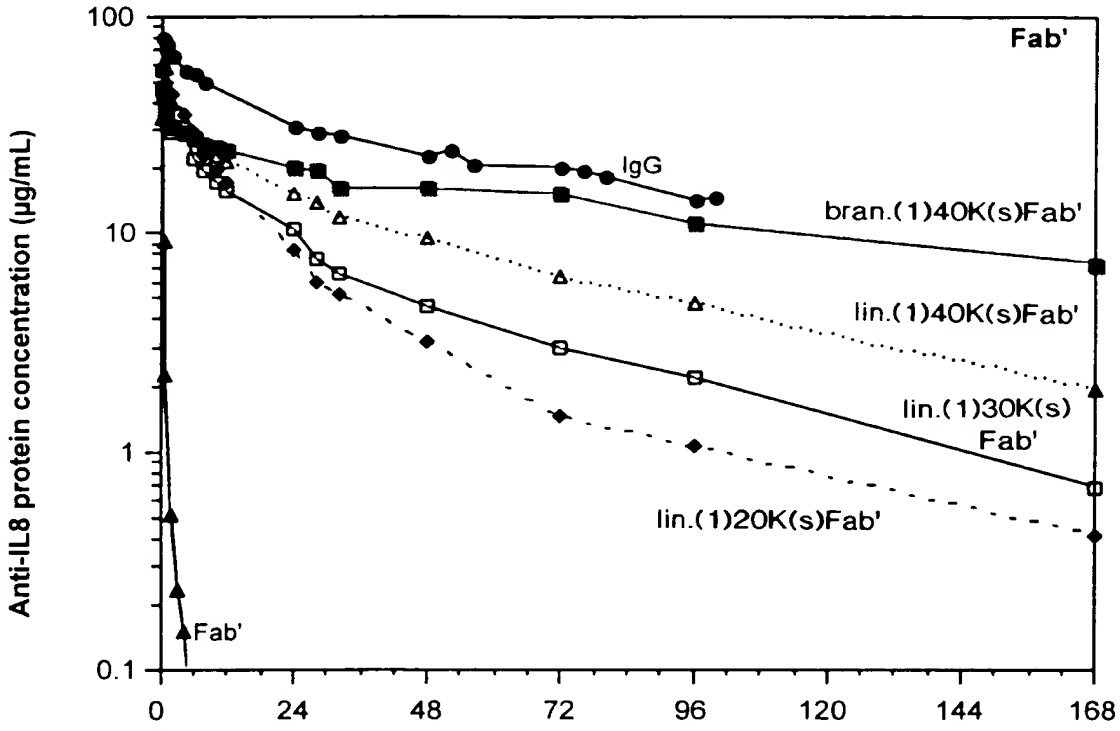


FIG. 65A

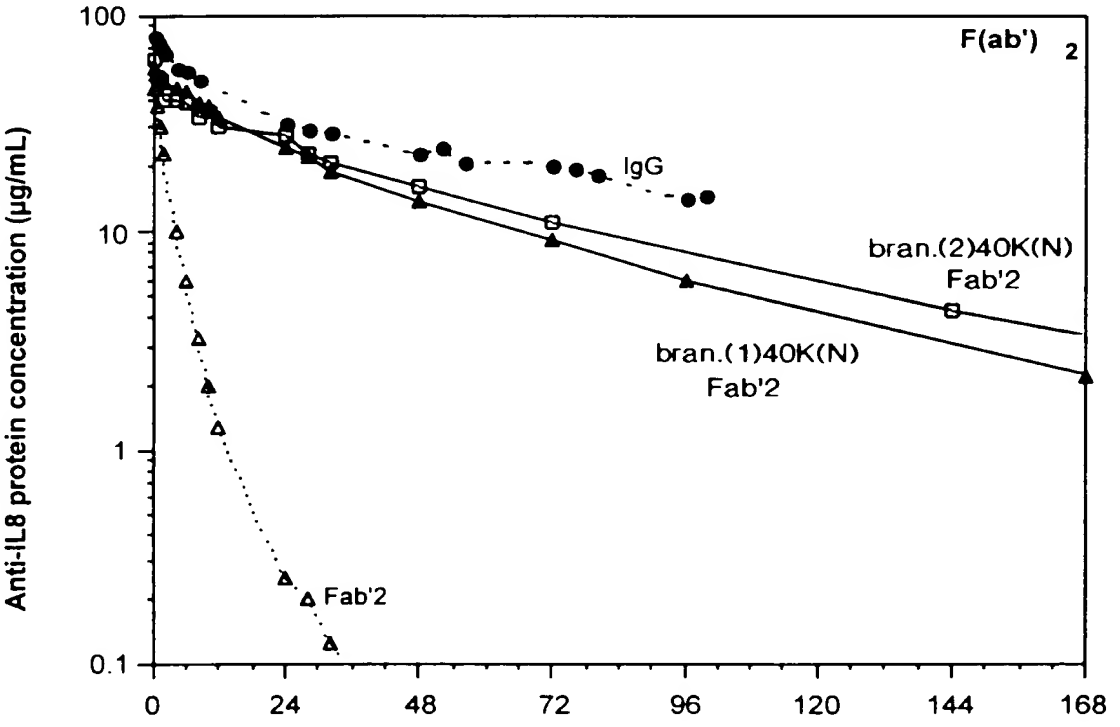


FIG. 65B

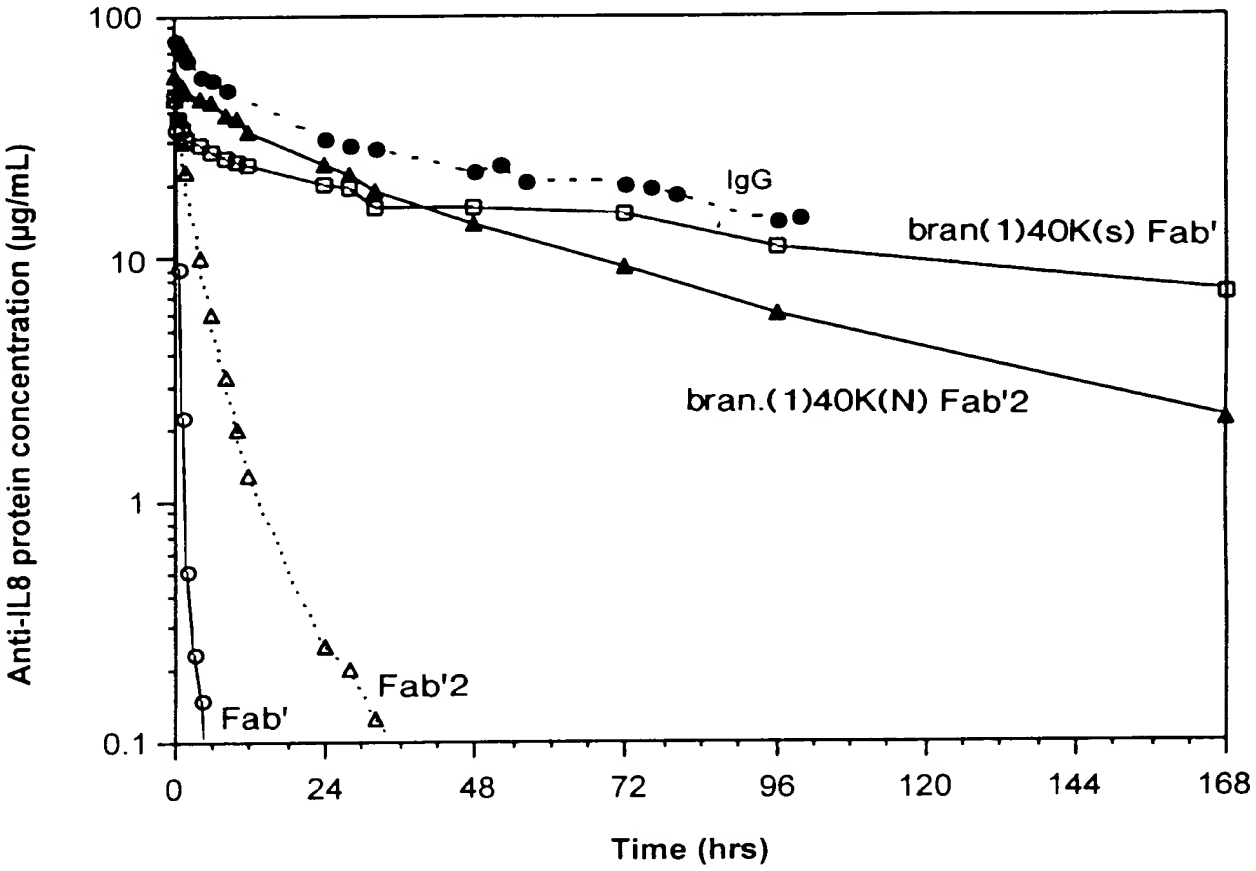


FIG. 66

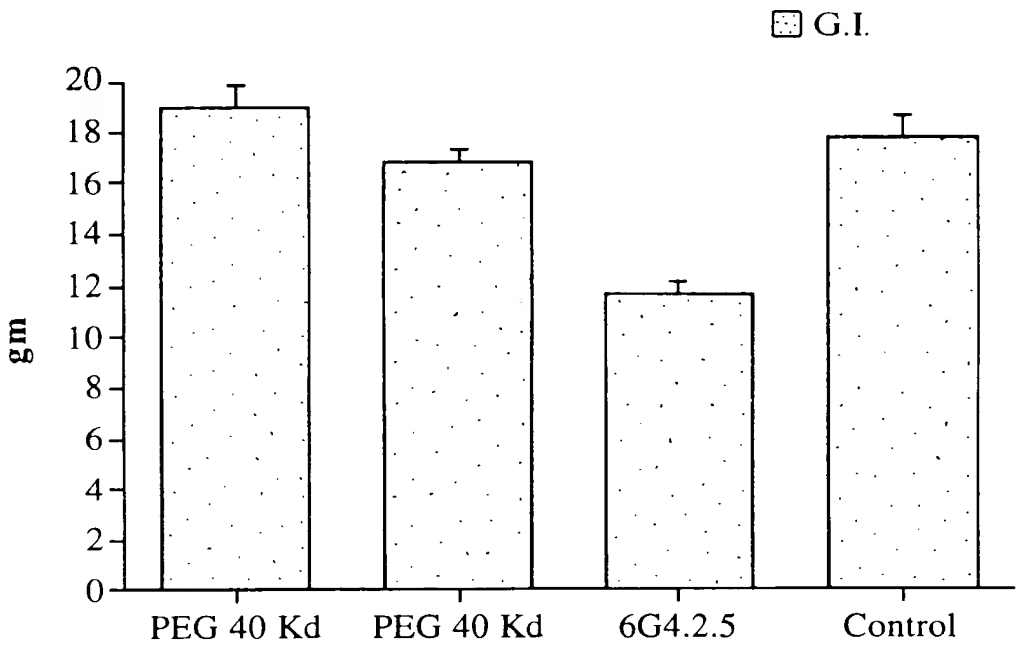


FIG. 67

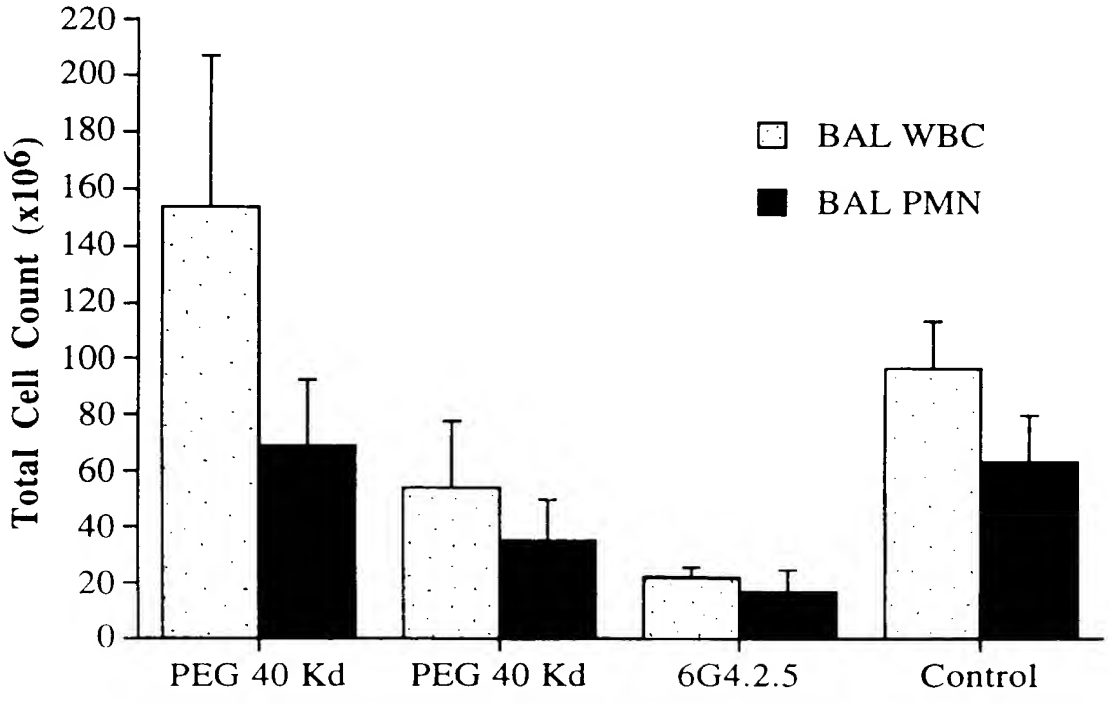


FIG. 68

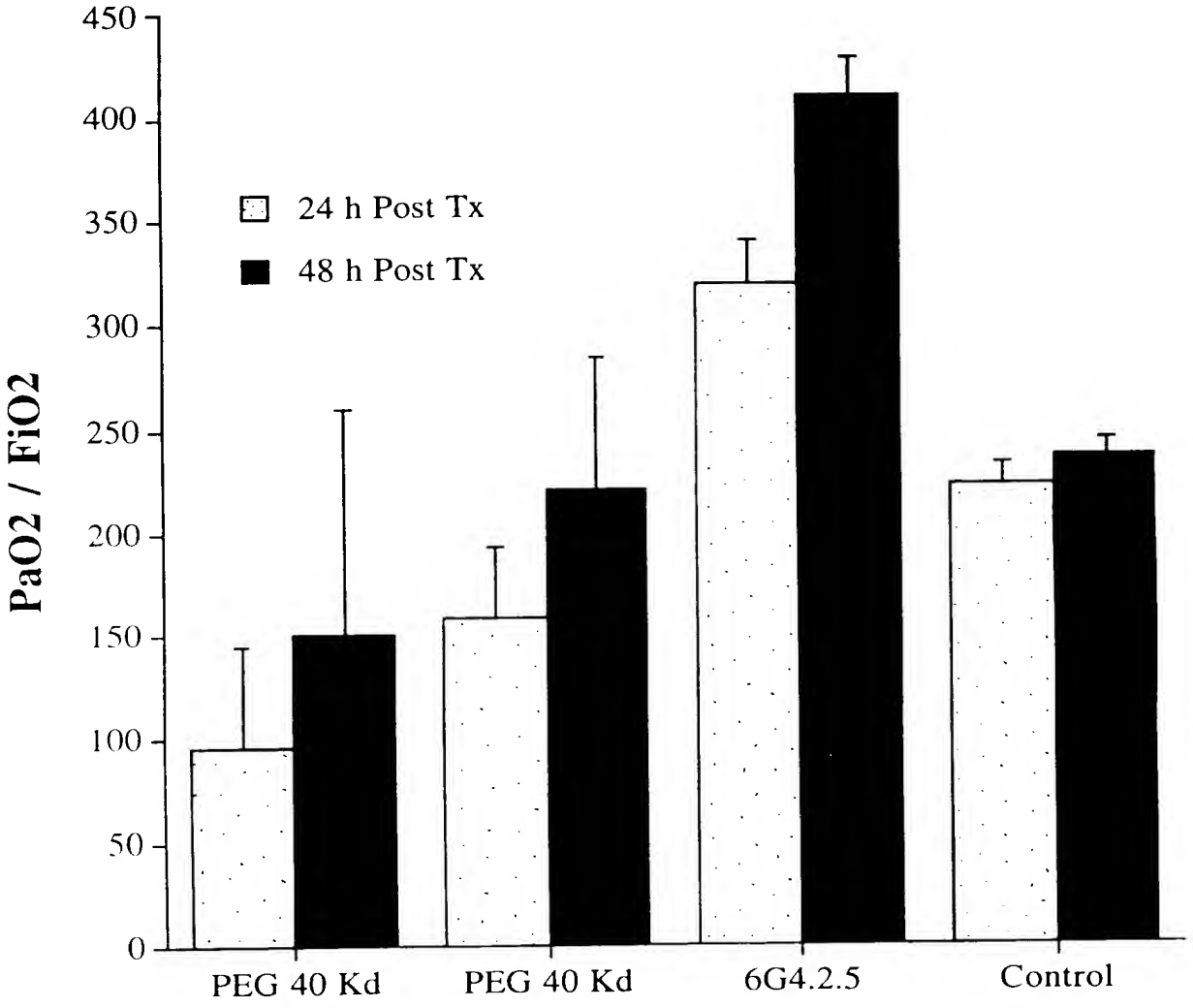


FIG. 69

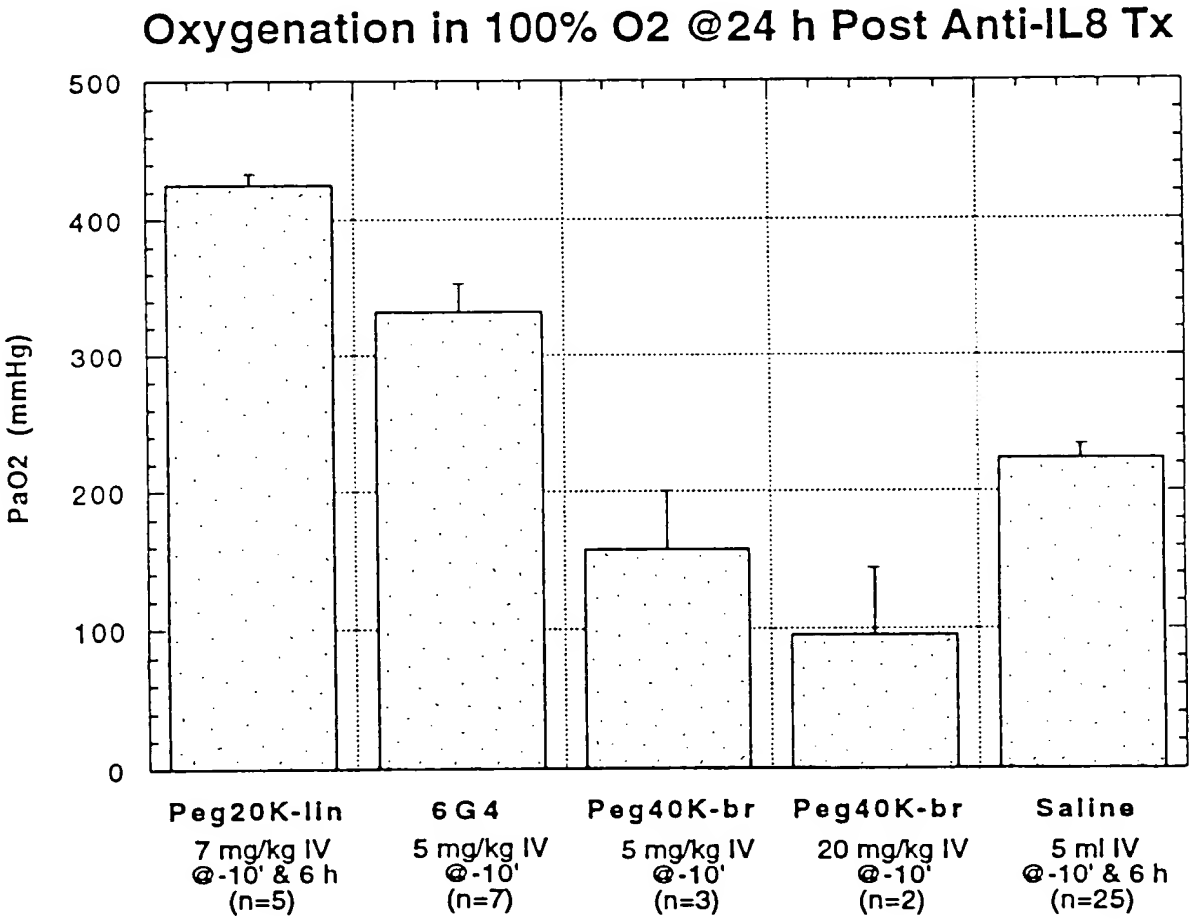


FIG. 70A

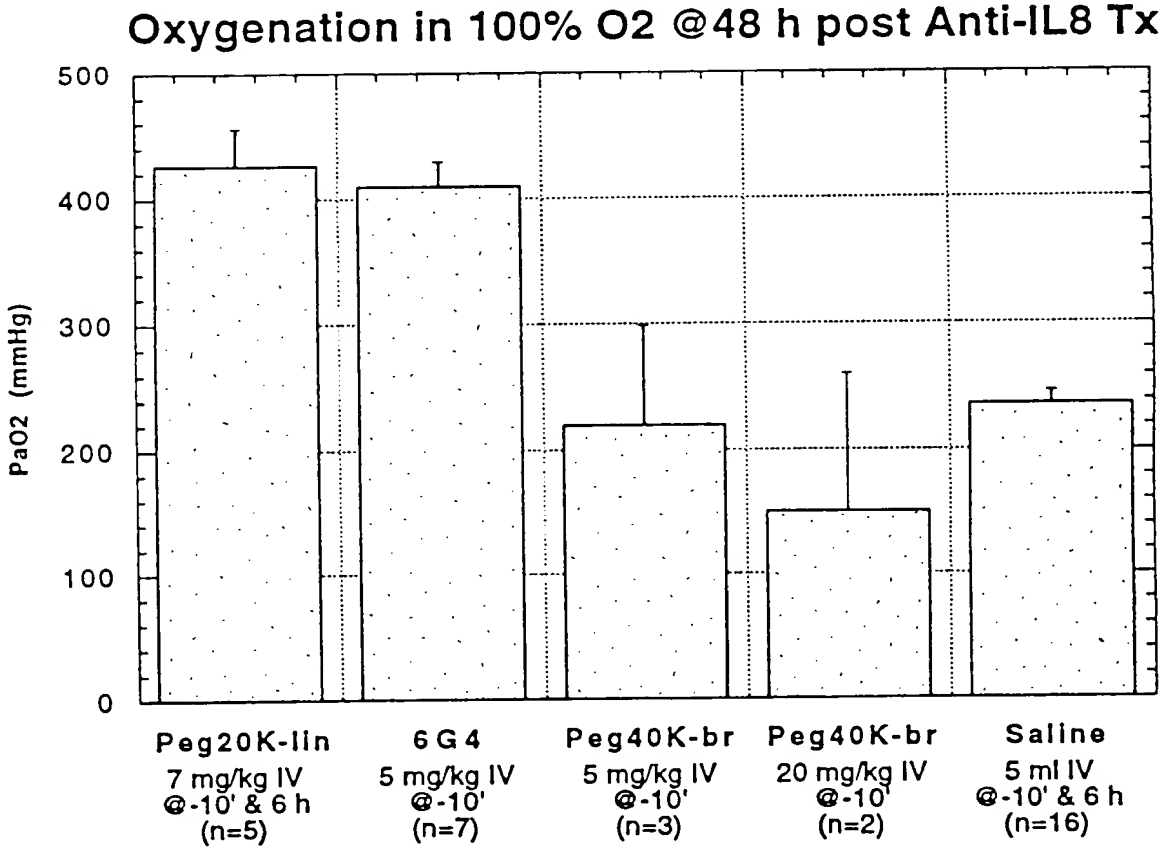


FIG. 70B

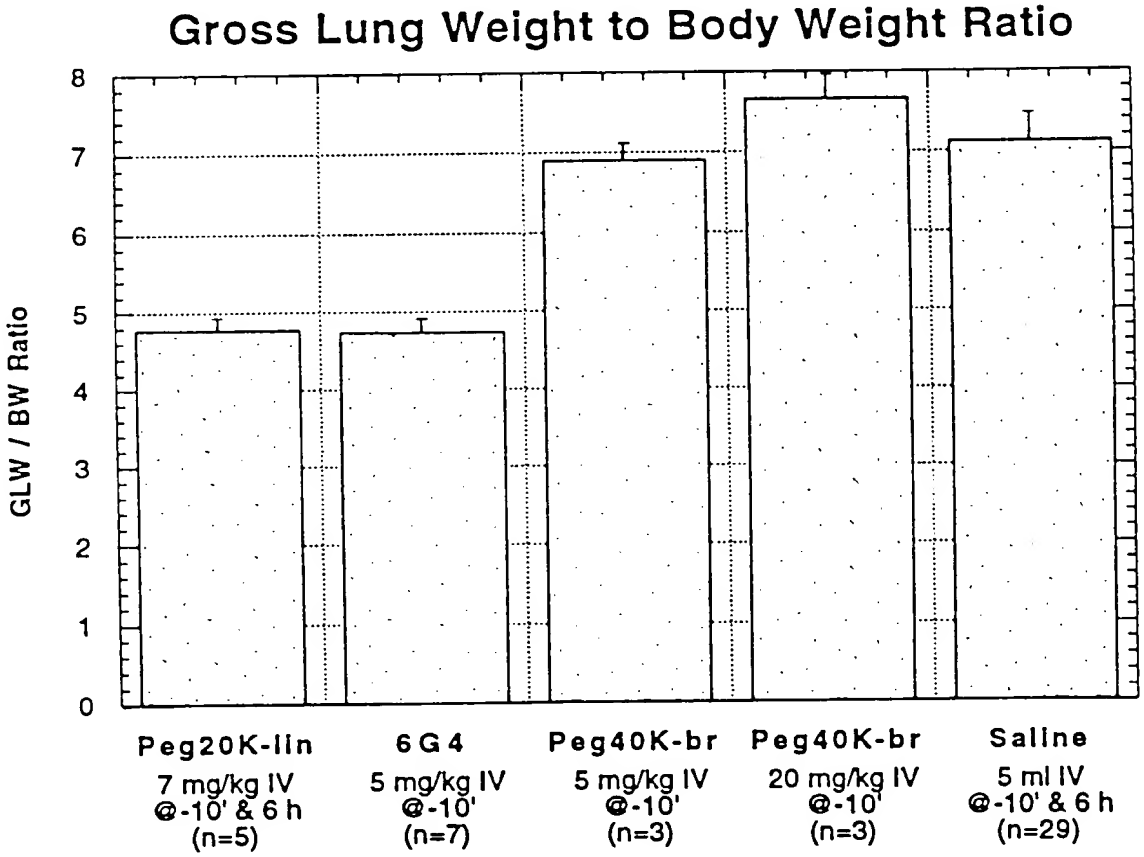


FIG. 70C

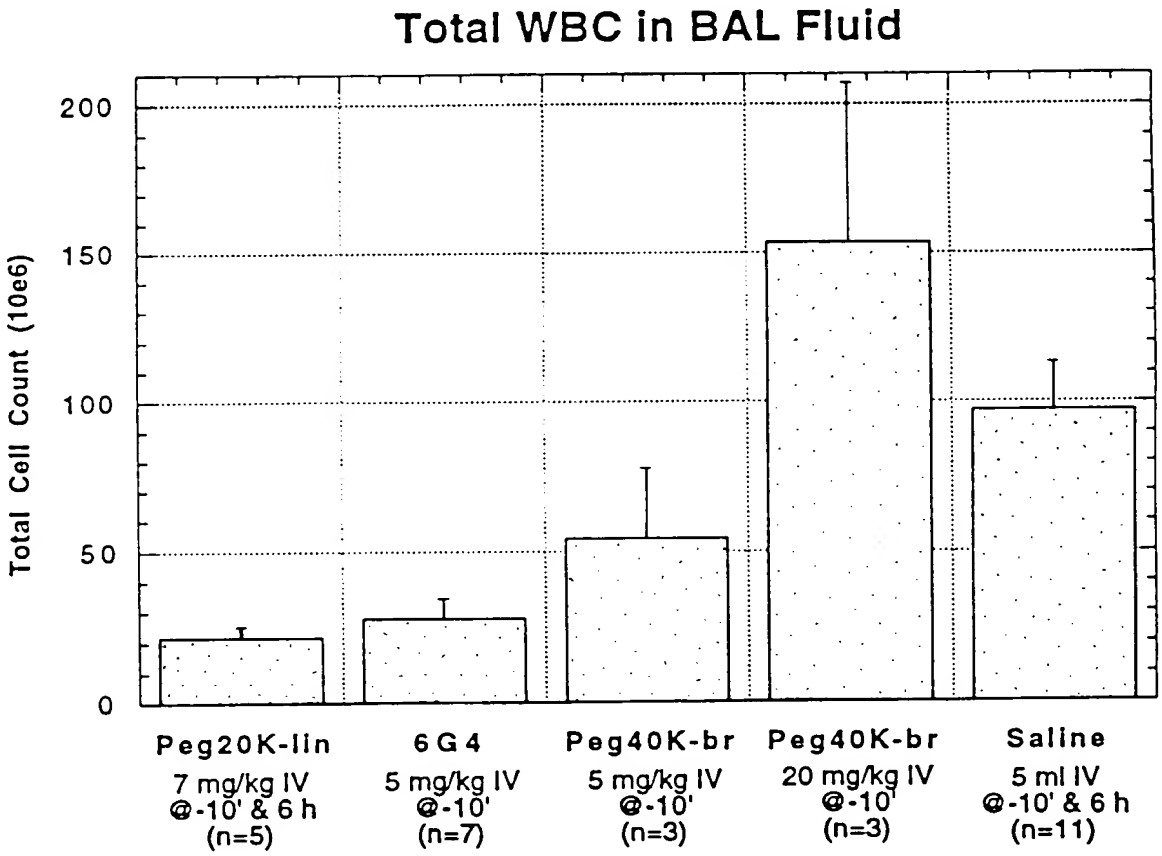


FIG. 70D

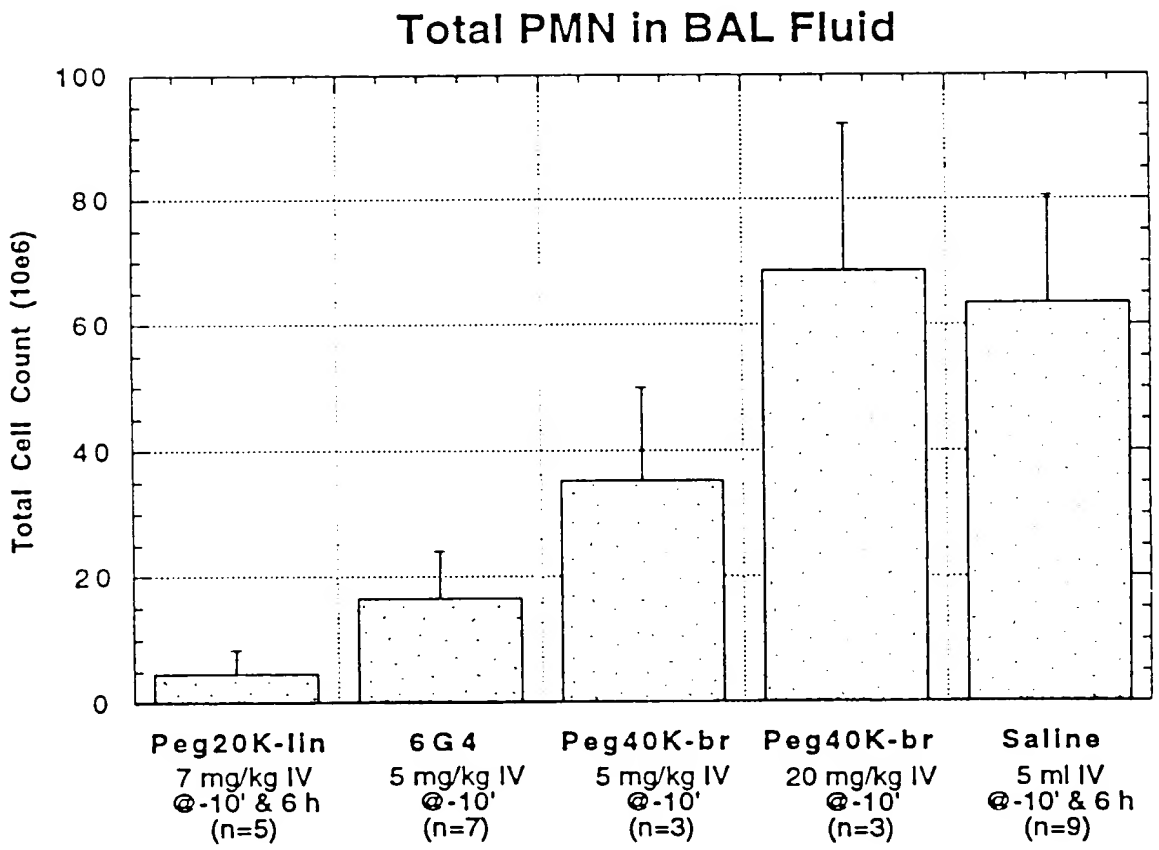
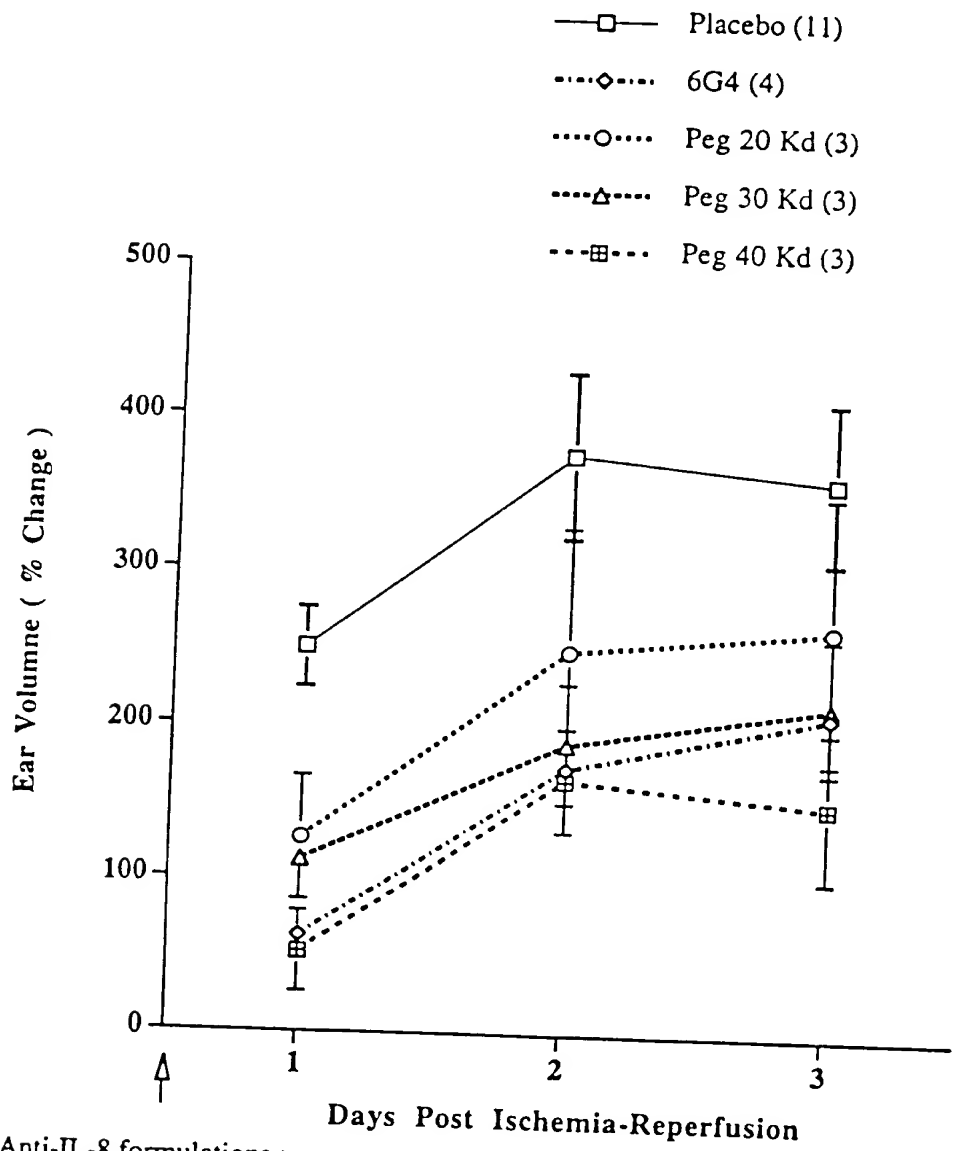

Total PMN in BAL Fluid
Total Cell Count (10e6)
100
80
60
40
20
0
Peg20K-lin
7 mg/kg IV
@-10' & 6 h
(n=5)
6G4
5 mg/kg IV
@-10'
(n=7)
Peg40K-br
5 mg/kg IV
@-10'
(n=3)
Peg40K-br
20 mg/kg IV
@-10'
(n=3)
Saline
5 ml IV
@-10' & 6 h
(n=9)

FIG. 70E

The Effect of Pegylated Anti-IL-8 in the Rabbit Ear model of Ischemia-Reperfusion Injury



Anti-IL-8 formulations : Single Dose (5 mg/kg) administered IV at time of reperfusion

FIG. 71